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TITLE

PROMOTERS FROM PLANT PROTOPORPHYRINOGEN OXIDASE GENES

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PROVISIONAL PATENT APPLICATION COVER SHEET

This is a request for filing a PROVISIONAL APPLICATION for patent under 37 CFR 1.53 (b)(2).

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TITLE OF THE INVENTION (280 characters max)

Promoters from Plant Protoporphyrinogen Oxidase Genes

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ENCLOSED APPLICATION PARTS (check all that apply)

- [x] 55 pages of Specification (and any claims)
- [x] 1 pages of Abstract (page 55)
- [ ] __ sheets of Drawing(s)
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Respectfully submitted,

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PROMOTERS FROM PLANT PROTOPORPHYRINOGEN OXIDASE GENES

CROSS-REFERENCE TO RELATED PROVISIONAL

This provisional application is related to U.S. provisional application serial no. 60/013,612 filed February 28, 1996.

FIELD OF THE INVENTION

This invention relates to novel DNA sequences which function as promoters of transcription of associated DNA sequences in plants. More specifically, this invention relates to novel promoters which are naturally associated with plant protoporphyrinogen oxidase (protox) coding sequences.

BACKGROUND OF THE INVENTION

1. The Protox Enzyme and its Involvement in the Chlorophyll/Heme Biosynthetic Pathway

The biosynthetic pathways which lead to the production of chlorophyll and heme share a number of common steps. Chlorophyll is a light harvesting pigment present in all green photosynthetic organisms. Heme is a cofactor of hemoglobin, cytochromes, P450 mixed-function oxygenases, peroxidases, and catalases (*see, e.g.* Lehninger, Biochemistry. Worth Publishers, New York (1975)), and is therefore a necessary component for all aerobic organisms.

The last common step in chlorophyll and heme biosynthesis is the oxidation of protoporphyrinogen IX to protoporphyrin IX. Protoporphyrinogen oxidase (referred to herein as "protox") is the enzyme which catalyzes this last oxidation step (Matringe *et al., Biochem. J. 260:* 231 (1989)).

The protox enzyme has been purified either partially or completely from a number of organisms including the yeast *Saccharomyces cerevisiae* (Labbe-Bois and Labbe, In Biosynthesis of Heme and Chlorophyll, E.H. Dailey, ed. McGraw Hill: New York, pp. 235-285 (1990)), barley etioplasts (Jacobs and Jacobs, *Biochem. J. 244:* 219 (1987)), and mouse liver (Dailey and Karr, *Biochem. 26:* 2697 (1987)). Genes encoding protox have been isolated from two prokaryotic

organisms, *Escherichia coli* (Sasarman *et al., Can. J. Microbiol. 39:* 1155 (1993)) and *Bacillus subtilis* (Dailey *et al., J. Biol. Chem. 269:* 813 (1994)). These genes share no sequence similarity; neither do their predicted protein products share any amino acid sequence identity. The *E. coli* protein is approximately 21 kDa, and associates with the cell membrane. The *B. subtilis* protein is 51 kDa, and is a soluble, cytoplasmic activity.

Protox encoding cDNAs have now also been isolated from humans (*see* Nishimura *et al., J. Biol. Chem. 270(14):* 8076-8080 (1995) and plants (International application no. PCT/IB95/00452 filed June 8, 1995, published Dec. 21, 1995 as WO 95/34659).

II. The Protox Gene as a Herbicide Target

The use of herbicides to control undesirable vegetation such as weeds or plants in crops has become almost a universal practice. The relevant market exceeds a billion dollars annually. Despite this extensive use, weed control remains a significant and costly problem for farmers.

Effective use of herbicides requires sound management. For instance, time and method of application and stage of weed plant development are critical to getting good weed control with herbicides. Since various weed species are resistant to herbicides, the production of effective herbicides becomes increasingly important.

Unfortunately, herbicides that exhibit greater potency, broader weed spectrum and more rapid degradation in soil can also have greater crop phytotoxicity. One solution applied to this problem has been to develop crops which are resistant or tolerant to herbicides. Crop hybrids or varieties resistant to the herbicides allow for the use of the herbicides without attendant risk of damage to the crop. Development of resistance can allow application of a herbicide to a crop where its use was previously precluded or limited (*e.g.* to pre-emergence use) due to sensitivity of the crop to the herbicide. For example, U.S. Patent No. 4,761,373 to Anderson *et al.* is directed to plants resistant to various imidazolinone or sulfonamide herbicides. The resistance is conferred by an altered acetohydroxyacid synthase (AHAS) enzyme. U.S. Patent No. 4,975,374 to Goodman *et al.* relates to plant cells and plants containing a gene encoding a mutant glutamine synthetase (GS) resistant to inhibition by herbicides that were known to inhibit GS, *e.g.*

phosphinothricin and methionine sulfoximine. U.S. Patent No. 5,013,659 to Bedbrook *et al.* is directed to plants that express a mutant acetolactate synthase which renders the plants resistant to inhibition by sulfonylurea herbicides. U.S. Patent No. 5,162,602 to Somers *et al.* discloses plants tolerant to inhibition by cyclohexanedione and aryloxyphenoxypropanoic acid herbicides. The tolerance is conferred by an altered acetyl coenzyme A carboxylase(ACCase).

The protox enzyme serves as the target for a variety of herbicidal compounds. The herbicides that inhibit protox include many different structural classes of molecules (Duke *et al.*, *Weed Sci.* 39: 465 (1991); Nandihalli *et al.*, *Pesticide Biochem. Physiol.* 43: 193 (1992); Matringe *et al.*, *FEBS Lett.* 245: 35 (1989); Yanase and Andoh, *Pesticide Biochem. Physiol.* 35: 70 (1989)). These herbicidal compounds include the diphenylethers (e.g. acifluorfen, 5-[2-chloro-4-(trifluoromethyl)phenoxy]-2-nitrobezoic acid; its methyl ester; or oxyfluorfen, 2-chloro-1-(3-ethoxy-4-nitrophenoxy)-4-(trifluorobenzene)), oxidiazoles, (e.g. oxidiazon, 3-[2,4-dichloro-5-(1-methylethoxy)phenyl]-5-(1,1-dimethylethyl)-1,3,4-oxadiazol-2-(3*H*)-one), cyclic imides (e.g. S-23142, *N*-(4-chloro-2-fluoro-5-propargyloxyphenyl)-3,4,5,6-tetrahydrophthalimide; chlorophthalim, *N*-(4-chlorophenyl)-3,4,5,6-tetrahydrophthalimide), phenyl pyrazoles (e.g. TNPP-ethyl, ethyl 2-[1-(2,3,4-trichlorophenyl)-4-nitropyrazolyl-5-oxy]propionate; M&B 39279), pyridine derivatives (e.g. LS 82-556), and phenopylate and its *O*-phenylpyrrolidino- and piperidinocarbamate analogs. Many of these compounds competitively inhibit the normal reaction catalyzed by the enzyme, apparently acting as substrate analogs.

Typically, the inhibitory effect on protox is determined by measuring fluorescence at about 622 to 635 nM, after excitation at about 395 to 410 nM (see, e.g. Jacobs and Jacobs, *Enzyme 28:* 206 (1982); Sherman *et al.*, *Plant Physiol.* 97: 280 (1991)). This assay is based on the fact that protoporphyrin IX is a fluorescent pigment, and protoporphyrinogen IX is nonfluorescent.

The predicted mode of action of protox-inhibiting herbicides involves the accumulation of protoporphyrinogen IX in the chloroplast. This accumulation is thought to lead to leakage of protoporphyrinogen IX into the cytosol where it is oxidized by a peroxidase activity to protoporphyrin IX. When exposed to light, protoporphyrin IX can cause formation of singlet oxygen in the cytosol. This singlet oxygen can in turn lead to the formation of other reactive

oxygen species, which can cause lipid peroxidation and membrane disruption leading to rapid cell death (Lee *et al.*, *Plant Physiol. 102*: 881 (1993)).

Not all protox enzymes are sensitive to herbicides which inhibit plant protox enzymes. Both of the protox enzymes encoded by genes isolated from *Escherichia coli* (Sasarman *et al.*, *Can. J. Microbiol. 39*: 1155 (1993)) and *Bacillus subtilis* (Dailey *et al.*, *J. Biol. Chem. 269*: 813 (1994)) are resistant to these herbicidal inhibitors. In addition, mutants of the unicellular alga *Chlamydomonas reinhardtii* resistant to the phenylimide herbicide S-23142 have been reported (Kataoka *et al.*, *J. Pesticide Sci. 15*: 449 (1990); Shibata *et al.*, In Research in Photosynthesis, Vol. III, N. Murata, ed. Kluwer:Netherlands, pp. 567-570 (1992)). At least one of these mutants appears to have an altered protox activity that is resistant not only to the herbicidal inhibitor on which the mutant was selected, but also to other classes of protox inhibitors (Oshio *et al.*, *Z. Naturforsch. 48c*: 339 (1993); Sato *et al.*, In ACS Symposium on Porphyric Pesticides, S. Duke, ed. ACS Press: Washington, D.C. (1994)). A mutant tobacco cell line has also been reported that is resistant to the inhibitor S-21432 (Che *et al.*, *Z. Naturforsch. 48c*: 350 (1993). In addition, modified, inhibitor-resistant forms of plant protox coding sequences have been described in international application no. PCT/IB95/00452 filed June 8, 1995, published Dec. 21, 1995 as WO 95/34659.

III. Regulation of Protox Gene Expression

The bulk of the research related to the protox gene which has been conducted thus far has focused upon the coding sequence and modifications to this enzyme which may render it resistant to protox inhibitors. No information is available in the art with regard to the regulatory elements which control and promote the expression of protox coding sequences in plants.

SUMMARY OF THE INVENTION

The present invention is based on the discovery that the promoter regions naturally associated with the plant protoporphyrinogen oxidase (protox) coding sequences, referred to herein generally as the "protox promoter", are useful for promoting expression of a heterologous coding sequence in a plant.

In accordance with this discovery, the present invention provides an isolated DNA molecule comprising a plant protox promoter. The present invention further provides a chimeric gene comprising a plant protox promoter operably linked to a heterologous coding sequence. Plant tissue and plants containing such a chimeric gene are also provided.

In one aspect of the invention the protox promoter is used to express herbicide resistant forms of herbicide target proteins in a plant to confer tolerance to the herbicide. According to this aspect, the protox promoter may be operably linked to a coding sequence for a herbicide-resistant plant protox protein which is resistant to inhibitors of unmodified plant protox protein.

DESCRIPTION OF THE SEQUENCE LISTING

SEQ ID No. 1: DNA coding sequence for an *Arabidopsis thaliana* protox-1 protein.

SEQ ID No. 2: *Arabidopsis thaliana* protox-1 amino acid sequence encoded by SEQ ID No. 1.

SEQ ID No. 3: DNA coding sequence for an *Arabidopsis thaliana* protox-2 protein.

SEQ ID No. 4: *Arabidopsis thaliana* protox-2 amino acid sequence encoded by SEQ ID No.3

SEQ ID No. 5: DNA coding sequence for a maize protox-1 protein.

SEQ ID No. 6: Maize protox-1 amino acid sequence encoded by SEQ ID No. 5

SEQ ID No. 7: DNA coding sequence for a maize protox-2 protein.

SEQ ID No. 8: Maize protox-2 amino acid sequence encoded by SEQ ID No. 7

SEQ ID No. 9: DNA coding sequence for a wheat protox-1 protein.

SEQ ID No. 10: Wheat protox-1 amino acid sequence encoded by SEQ ID No. 9.

SEQ ID No. 11: DNA coding sequence for a soybean protox-1 protein.

SEQ ID No. 12: Soybean protox-1 protein encoded by SEQ ID No. 11.

SEQ ID NO. 13: Promoter sequence from *Arabidopsis thaliana* protox-1 gene.

SEQ ID NO. 14: Promoter sequence from *Zea mays* (maize) protox-1 gene.

DEFINITIONS

As used herein a "plant protox promoter" is used to refer to the regulatory region which naturally occurs immediately upstream of a protoporphyrinogen oxidase (protox) coding sequence in a plant and is responsible, in its naturally occurring state, for regulating the transcription of the associated protox coding sequence. The plant protox promoter includes the DNA region directly involved in binding of RNA polymerase to initiate transcription and additional upstream regulatory cis-elements which influence the transcription of an operably linked coding sequence.

As used herein a "gene" is used to refer to a DNA molecule which includes (1) a coding sequence and (2) associated regulatory regions which promote and regulate the transcription of the coding sequence in a suitable host cell. The coding sequence may encode a useful transcript (e.g. antisense RNA) or polypeptide produced by translation of the encoded transcript. A gene includes at a minimum, in 5'-3' orientation, a promoter region, a coding sequence and a transcription terminator. A gene may also include additional regulatory regions which can occur as part of the minimal elements (e.g. leaders or signal peptides within the coding sequence) or as discrete elements (e.g. introns).

As used herein a "chimeric gene" refers to a gene which does not naturally occur wherein at least one component part is heterologous with respect to another component part. As used herein to describe the present invention a "chimeric gene" refers to a gene which includes the promoter of the invention operably linked to a heterologous coding sequence.

As used herein with reference to the relationship between a promoter and a coding sequence, the term "heterologous" is used to refer to a relationship which does not naturally occur. For instance, a coding sequence is considered heterologous with respect to a promoter sequence if it is different from the coding sequence that naturally occurs in association with the promoter sequence. This includes modified forms of coding sequences which are naturally associated with a subject promoter. Accordingly, a modified, inhibitor-resistant protox coding sequence is considered to be heterologous with respect to the promoter that is naturally associated with the unmodified, inhibitor-sensitive form of this coding sequence.

As used herein, the term "substantial sequence homology" is used to indicate that a nucleotide sequence (in the case of DNA or RNA) or an amino acid sequence (in the case of a protein or polypeptide) exhibits substantial structural and functional equivalence with another nucleotide or amino acid sequence. Any functional or structural differences between sequences having substantial sequence homology will be de minimis; that is they will not affect the ability of the sequence to function as indicated in the present application. For example, a sequence which has substantial sequence homology with a DNA sequence disclosed to be a plant protox promoter will be able to direct the same level and pattern of expression of an associated DNA sequence as the plant protox promoter. Sequences that have substantial sequence homology with the sequences disclosed herein are usually variants of the disclosed sequence, such as mutations, but may also be synthetic sequences. Structural differences are considered de minimis if there is a significant amount of sequence overlap or similarity between two or more different sequences or if the different sequences exhibit similar physical characteristics. Such characteristics can include, for example, immunological reactivity, enzyme activity, structural protein integrity, etc.

Two nucleotide sequences may have substantial sequence homology if the sequences have at least 70 percent, more preferably 80 percent and most preferably 90 percent sequence similarity between them. Two amino acid sequences have substantial sequence homology if they have at least 50 percent, preferably 70 percent, and most preferably 90 percent similarity between the active portions of the polypeptides. In the case of promoter DNA sequences, "substantial sequence homology" also refers to those fragments of a promoter DNA sequence that are able to operate to promote the expression of associated DNA sequences. Such operable fragments of a promoter DNA sequence may be derived from the promoter DNA sequence, for example, by cleaving the promoter DNA sequence using restriction enzymes, synthesizing in accordance with the sequence of the promoter DNA sequence, or may be obtained through the use of PCR technology. Mullis et al., Meth. Enzymol., 155:335-350 (1987); Erlich (ed.), PCR Technology, Stockton Press (New York 1989).

A promoter DNA sequence is said to be "operably linked" to a second DNA sequence if the two are situated such that the promoter DNA sequence influences the transcription or translation of the second DNA sequence. For example, if the second DNA sequence codes for

the production of a protein, the promoter DNA sequence would be operably linked to the second DNA sequence if the promoter DNA sequence affects the expression of the protein product from the second DNA sequence. For example, in a DNA sequence comprising a promoter DNA sequence physically attached to a coding DNA sequence in the same chimeric construct, the two sequences are likely to be operably linked.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to promoter DNA sequences which are naturally associated with coding sequences for plant protoporphyrinogen oxidase (referred to herein as "protox"; *see* international application no. PCT/IB95/00452 filed June 8, 1995, published Dec. 21, 1995 as WO 95/34659 and co-pending provisional application entitled " DNA Molecules Encoding Plant Protoporphyrinogen Oxidase and Inhibitor Resistant Mutants Thereof" filed on the same day as the instant application). These protox promoter sequences have been found to be useful for the expression of a heterologous coding sequence in a plant.

The promoter sequence for the *Arabidopsis thaliana* protox-1 coding sequence (SEQ ID No. 1) is provided as SEQ ID No. 13. Isolation of this promoter from a genomic library using the associated coding sequence as a probe is described in Example 1. The promoter sequence for the maize protox-1 coding sequence (SEQ ID No. 5) is provided as SEQ ID No. 14. Isolation of this promoter from a genomic library using the associated coding sequence as a probe is described in Example 4.

The approach used to isolate the *Arabidopsis* and maize protox-1 promoters can be used to isolate the promoter sequence from any plant protox gene. Any protox coding sequence which shares sufficient homology to hybridize to the protox coding sequence associated with the promoter of interest may be used as a probe in this approach. Since the respective protox-1 and protox-2 coding sequences from all plants are contemplated to share this requisite degree of homology, the choice of which protox coding sequence is used as a probe is not considered critical. However, for optimal hybridization results it is preferable to use the most closely related protox coding sequence. Most preferably, the coding sequence used as a probe is from the same

plant species as the protox promoter of interest and is the coding sequence naturally associated with the promoter.

The plant protox promoter of the present invention includes the *Arabidopsis* protox-1 promoter sequence set forth in SEQ Id No. 13 as well as corresponding protox-1 promoter sequences available from other plant species as indicated above. The present invention also includes functional fragments of these DNA sequences which retain the ability to regulate expression of an operably linked coding sequence in the same manner as the exemplified protox promoter sequence. Such functional fragments may be identified through deletion analyses or other standard techniques used in the art to identify protox promoter activity (*see, e.g.* pages 546-549 of "Genes IV", ed. by Lewin, Oxford Univ. Press (1990)). The present invention also includes DNA sequences having substantial sequence homology with the protox promoters available from plant genes which confer an equivalent level and pattern of expression upon an operably linked sequence. Such promoter sequences may be obtained through modification of the protox promoters isolated from plant genes and are considered functionally equivalent derivatives of the plant protox promoters.

As illustrated in the examples below, the DNA sequences, vectors and transgenic plants of the present invention comprise a promoter sequence derived from a plant protox gene. The protox promoter DNA sequences are preferably linked operably to a coding DNA sequence, for example a DNA sequence which is transcribed into a useful RNA transcript such as an antisense transcript, or a coding sequence which is ultimately expressed in the production of a useful protein product.

In a preferred embodiment, the protox promoter is used to direct the expression of a modified herbicide target enzyme which is resistant to herbicides at levels that inhibit the corresponding unmodified version of the enzyme. Such modified herbicide-resistant enzymes include herbicide-resistant forms of imidazoleglycerol phosphate dehyratase (IGPD; *see* WO 9426909 published Nov. 24, 1994), EPSP synthase (*see* U.S. Pat. Nos. 4,535,060; 4,769,061; 4,940,835 and EP 550,633), glutamine synthetase (GS; *see* U.S. Patent No. 4,975,374), acetyl coenzyme A carboxylase ACCase; *see* U.S. Patent No. 5,162,602), and acetolactate synthase (*see* U.S. Patent Nos. 4,761,373; 5,304,732; 5,331,107; 5,013,659; 5,141,870; and 5,378,824).

In a most preferred embodiment, the protox promoter is used to direct the expression of a modified protox enzyme which is resistant to protox inhibitors as illustrated in Examples 2-3 (*see also* International application no. PCT/IB95/00452 filed June 8, 1995, published Dec. 21, 1995 as WO 95/34659 whose relevant parts are herein incorporated by reference; *see also* co-pending application entitled " DNA Molecules Encoding Plant Protoporphyrinogen Oxidase and Inhibitor Resistant Mutants Thereof" filed on the same day as the instant application).

The transgenic plants of the present invention may be transformed by any method of transformation known in the art. These methods include, for instance, transformation by direct infection or co-cultivation of plants, plant tissue or cells with *Agrobacterium tumefaciens*; Horsch *et al., Science. 225:* 1229 (1985); Marton, "Cell Culture and Somatic Cell Genetic of Plants", vol 1, pp 514-521 (1984); direct gene transfer into protoplasts; Paszkowski *et al., EMBO J. 12:* 2717 (1984); Loerz *et al., Mol. Gen. & Genet. 1199*:178 (1985); Fromm *et al., Nature 319*:719 (1986); microprojectile bombardment, Klein *et al., Bio/Technology*, 6:559-563 (1988); injection into protoplasts cultured cells and tissues, Reich *et al., Bio/Technology*, 4:1001-1004 (1986); or injection into meristematic tissues of seedlings and plants as described by De La Pena *et al., Nature, 325*:274-276 (1987); Hooykaas-Van Slogteren *et al., Nature, 311*:763-764 (1984); Grimsley *et al., Bio/Technology*, 6:185 (1988); and Grimsley *et al., Nature, 325*:177 (1988).

The invention is illustrated in more detail by the following examples, without implying any restriction to what is described therein.

EXAMPLES

EXAMPLE 1: Isolation of the Arabidopsis thaliana Protox-1 promoter sequence

A Lambda Zap II genomic DNA library prepared from *Arabidopsis thaliana* (Columbia, whole plant) was purchased from Stratagene. Approximately 125,000 phage were plated at a density of 25,000 pfu (plaque forming units) per 15 cm Petri dish and duplicate lifts were made onto Colony/Plaque Screen membranes (NEN Dupont). The plaque lifts were probed with the Arabidopsis Protox-1 cDNA (SEQ ID No. 1 labeled with 32P-dCTP by the random priming method (Life Technologies). Hybridization and wash conditions were at 65° C as described in Church and Gilbert, *Proc. Natl. Acad. Sci. USA 81:* 1991-1995 (1984). Positively hybridizing plaques were purified and *in vivo* excised into pBluescript plasmids. Sequence from the genomic DNA inserts was determined by the chain termination method using dideoxy terminators labeled with fluorescent dyes (Applied Biosystems, Inc.). One clone, AraPT1Pro, was determined to contain 580 bp of Arabidopsis sequence upstream from the initiating methionine (ATG) of the Protox-1 protein coding sequence. This clone also contains coding sequence and introns that extend to bp 1241 of the Protox-1 cDNA sequence. The 580 bp 5 noncoding fragment is the putative Arabidopsis Protox-1 promoter, and the sequence is set forth in SEQ ID No. 13.

AraPT1Pro was deposited December 14, 1995, as pWDC-11 (NRRL #B-21515)

EXAMPLE 2: Construction of plant transformation vectors expressing altered Protox-1 genes behind the native Arabidopsis Protox-1 promoter

A full-length cDNA of the appropriate altered *Arabidopsis* Protox-1 cDNA is isolated as an EcoRI-XhoI partial digest fragment and cloned into the plant expression vector pCGN1761ENX (see Example 9 of International application no. PCT/IB95/00452 filed June 8, 1995, published Dec. 21, 1995 as WO 95/34659). This plasmid is digested with NcoI and BamHI to produce a fragment comprised of the complete Protox-1 cDNA plus a transcription terminator from the 3' untranslated sequence of the tml gene of *Agrobacterium tumefaciens*. The AraPT1Pro plasmid described above is digested with NcoI and BamHI to produce a fragment comprised of pBluescript and the 580 bp putative Arabidopsis Protox-1 promoter. Ligation of these two fragments produces a fusion of the ltered protox cDNA to the native protox promoter.

The expression cassette containing the Protox-1 promoter/Protox-1 cDNA/tml terminator fusion is excised by digestion with KpnI and cloned into the binary vector pCIB200. The binary plasmid is transformed by electroporation into Agrobacterium and then into Arabidopsis using the vacuum infiltration method (Bechtold *et al. C.R. Acad. Sci. Paris 316:* 1194-1199 (1993)). Transformants expressing altered protox genes are selected on kanamycin or on various concentrations of protox inhibiting herbicide.

EXAMPLE 3: Production of herbicide tolerant plants by expression of a native Protox-1 promoter/altered Protox-1 fusion

Using the procedure described above, an *Arabidopsis* Protox-1 cDNA containing a TAC to ATG (Tyrosine to Methionine) change at nucleotides 1306-1308 in the Protox-1 sequence (SEQ ID No.1) was fused to the native Protox-1 promoter fragment and transformed into *Arabidopsis thaliana*. This altered Protox-1 enzyme (AraC-2Met) has been shown to be >10fold more tolerant to various protox-inhibiting herbicides than the naturally occurring enzyme when tested in a bacterial expression system (*see* Example 5 of copending U.S. application entitled " DNA Molecules Encoding Plant Protoporphyrinogen Oxidase and Inhibitor Resistant Mutants Thereof" filed on the same day as the instant application). Seed from the vacuum infiltrated plants was collected and plated on a range (10.0nM-1.0uM) of a protox inhibitory aryluracil herbicide of formula XVII. Multiple experiments with wild type *Arabidopsis* have shown that a 10.0nM concentration of this compound is sufficient to prevent normal seedling germination. Transgenic seeds expressing the AraC-2Met altered enzyme fused to the native Protox-1 promoter produced normal Arabidopsis seedlings at herbicide concentrations up to 500nM, indicating at least 50-fold higher herbicide tolerance when compared to wild-type Arabidopsis. This promoter/altered protox enzyme fusion therefore functions as an effective selectable marker for plant transformation. Several of the plants that germinated on 100.0nM of protox-inhibiting herbicide were transplanted to soil, grown 2-3 weeks, and tested in a spray assay with various concentrations of the protox-inhibiting herbicide. When compared to empty vector control transformants, the AraPT1Pro/AraC-2Met transgenics were >10fold more tolerant to the herbicide spray.

EXAMPLE 4: Isolation of a Maize Protox-1 promoter sequence

A Zea Mays (Missouri 17 inbred, etiolated seedlings) genomic DNA library in the Lambda FIX II vector was purchased from Stratagene. Approximately 250,000 pfu of the library was plated at a density of 50,000 phage per 15 cm plate and duplicate lifts were made onto Colony/Plaque screen membranes (NEN Dupont). The plaque lifts were probed with the maize Protox-1 cDNA labeled with 32P-dCTP by the random priming method (Life Technologies). Hybridization and wash conditions were at 65o C as described in Church and Gilbert, *Proc. Natl. Acad. Sci. USA 81:* 1991-1995 (1984). Lambda phage DNA was isolated from three positively hybridizing phage using the Wizard Lambda Preps DNA Purification System (Promega). Analysis by restriction digest, hybridization patterns, and DNA sequence analysis identified a lambda clone containing approximately 3.5 kb of maize genomic DNA located 5' to the maize Protox-1 coding sequence previously isolated as a cDNA clone. This fragment is contemplated to include the maize Protox-1 promoter. The sequence of this fragment is set forth in SEQ ID NO 14. From nucleotide 1 to 3532, this sequence is comprised of 5' noncoding sequence. From nucleotide 3533 to 3848, this sequence encodes the 5' end of the maize Protox-1 protein.

A plasmid containing the sequence of SEQ ID NO. 14 fused to the remainder of the maize Protox-1 coding sequence was deposited March 19, 1996 as pWDC-14 (NRRL #B-21546).

EXAMPLE 5: Construction of Plant Transformation Vectors

Numerous transformation vectors are available for plant transformation, and the promoters and chimeric genes of this invention can be used in conjunction with any such vectors. The selection of vector for use will depend upon the preferred transformation technique and the target species for transformation. For certain target species, different antibiotic or herbicide selection markers may be preferred. Selection markers used routinely in transformation include the *nptII* gene which confers resistance to kanamycin and related antibiotics (Messing & Vierra, *Gene 19:* 259-268 (1982); Bevan *et al., Nature 304:*184-187 (1983)), the *bar* gene which confers resistance to the herbicide phosphinothricin (White *et al., Nucl Acids Res 18:* 1062 (1990), Spencer *et al.* Theor Appl Genet 79: 625-631(1990)), the *hph* gene which confers resistance to

the antibiotic hygromycin (Blochinger & Diggelmann, *Mol Cell Biol 4*: 2929-2931), and the *dhfr* gene, which confers resistance to methotrexate (Bourouis *et al.*, *EMBO J.* 2(7): 1099-1104 (1983)).

(1) Construction of Vectors Suitable for *Agrobacterium* Transformation

Many vectors are available for transformation using *Agrobacterium tumefaciens*. These typically carry at least one T-DNA border sequence and include vectors such as pBIN19 (Bevan, *Nucl. Acids Res.* (1984)) and pXYZ. Below the construction of two typical vectors is described.

Construction of pCIB200 and pCIB2001

The binary vectors pCIB200 and pCIB2001 are used for the construction of recombinant vectors for use with *Agrobacterium* and was constructed in the following manner. pTJS75kan was created by *NarI* digestion of pTJS75 (Schmidhauser & Helinski, *J Bacteriol. 164*: 446-455 (1985)) allowing excision of the tetracycline-resistance gene, followed by insertion of an *AccI* fragment from pUC4K carrying an NPTII (Messing & Vierra, *Gene 19*: 259-268 (1982); Bevan *et al.*, *Nature 304*: 184-187 (1983); McBride *et al.*, *Plant Molecular Biology 14*: 266-276 (1990)). *XhoI* linkers were ligated to the *EcoRV* fragment of pCIB7 which contains the left and right T-DNA borders, a plant selectable *nos/nptII* chimeric gene and the pUC polylinker (Rothstein *et al.*, *Gene 53*: 153-161 (1987)), and the *XhoI*-digested fragment was cloned into *SalI*-digested pTJS75kan to create pCIB200 (see also EP 0 332 104, example 19 [1338]). pCIB200 contains the following unique polylinker restriction sites: *EcoRI*, *SstI*, *KpnI*, *BglII*, *XbaI*, and *SalI*. *pCIB2001* is a derivative of pCIB200 which created by the insertion into the polylinker of additional restriction sites. Unique restriction sites in the polylinker of pCIB2001 are *EcoRI*, *SstI*, *KpnI*, *BglII*, *XbaI*, *SalI*, *MluI*, *BclI*, *AvrII*, *ApaI*, *HpaI*, and *StuI*. pCIB2001, in addition to containing these unique restriction sites also has plant and bacterial kanamycin selection, left and right T-DNA borders for *Agrobacterium*-mediated transformation, the RK2-derived *trfA* function

for mobilization between *E. coli* and other hosts, and the *OriT* and *OriV* functions also from RK2. The pCIB2001 polylinker is suitable for the cloning of plant expression cassettes containing their own regulatory signals.

Construction of pCIB10 and Hygromycin Selection Derivatives thereof

The binary vector pCIB10 contains a gene encoding kanamycin resistance for selection in plants, T-DNA right and left border sequences and incorporates sequences from the wide host-range plasmid pRK252 allowing it to replicate in both *E. coli* and *Agrobacterium*. Its construction is described by Rothstein *et al.*, *Gene 53*: 153-161 (1987). Various derivatives of pCIB10 have been constructed which incorporate the gene for hygromycin B phosphotransferase described by Gritz *et al.*, *Gene 25*: 179-188 (1983)). These derivatives enable selection of transgenic plant cells on hygromycin only (pCIB743), or hygromycin and kanamycin (pCIB715, pCIB717).

(2) Construction of Vectors Suitable for non-*Agrobacterium* Transformation.

Transformation without the use of *Agrobacterium tumefaciens* circumvents the requirement for T-DNA sequences in the chosen transformation vector and consequently vectors lacking these sequence: can be utilized in addition to vectors such as the ones described above which contain T-DNA sequences. Transformation techniques which do not rely on *Agrobacterium* include transformation via particle bombardment, protoplast uptake (*e.g.* PEG and electroporation) and microinjection. The choice of vector depends largely on the preferred selection for the species being *transformed*. Below, the construction of some typical vectors is described.

Construction of pCIB3064

pCIB3064 is a pUC-derived vector suitable for direct gene transfer techniques in combination with selection by the herbicide basta (or phosphinothricin). The plasmid pCIB246

comprises the CaMV 35S promoter in operational fusion to the *E. coli* GUS gene and the CaMV 35S transcriptional terminator and is described in the PCT published application WO 93/07278. The 35S promoter of this vector contains two ATG sequences 5' of the start site. These sites were mutated using standard PCR techniques in such a way as to remove the ATGs and generate the restriction sites *SspI* and *PvuII*. The new restriction sites were 96 and 37 bp away from the unique *SalI* site and 101 and 42 bp away from the actual start site. The resultant derivative of pCIB246 was designated pCIB3025. The GUS gene was then excised from pCIB3025 by digestion with *SalI* and *SacI*, the termini rendered blunt and religated to generate plasmid pCIB3060. The plasmid pJIT82 was obtained from the John Innes Centre, Norwich and the 400 bp *SmaI* fragment containing the *bar* gene from *Streptomyces viridochromogenes* was excised and inserted into the *HpaI* site of pCIB3060 (Thompson *et al.* EMBO J 6: 2519-2523 (1987)). This generated pCIB3064 which comprises the *bar* gene under the control of the CaMV 35S promoter and terminator for herbicide selection, a gene fro ampicillin resistance (for selection in *E. coli*) and a polylinker with the unique sites *SphI, PstI, HindIII,* and *BamHI*. This vector is suitable for the cloning of plant expression cassettes containing their own regulatory signals.

Construction of pSOG19 and pSOG35

pSOG35 is a transformation vector which utilizes the *E. coli* gene dihydrofolate reductase (DHFR) as a selectable marker conferring resistance to methotrexate. PCR was used to amplify the 35S promoter (~800 bp), intron 6 from the maize Adh1 gene (~550 bp) and 18 bp of the GUS untranslated leader sequence from pSOG10. A 250 bp fragment encoding the *E. coli* dihydrofolate reductase type II gene was also amplified by PCR and these two PCR fragments were assembled with a *SacI-PstI* fragment from pBI221 (Clontech) which comprised the pUC19 vector backbone and the nopaline synthase terminator. Assembly of these fragments generated pSOG19 which contains the 35S promoter in fusion with the intron 6 sequence, the GUS leader, the DHFR gene and the nopaline synthase terminator. Replacement of the GUS leader in

pSOG19 with the leader sequence from Maize Chlorotic Mottle Virus (MCMV) generated the vector pSOG35. pSOG19 and pSOG35 carry the pUC gene for ampicillin resistance and have *HindIII*, *SphI*, *PstI* and *EcoRI* sites available for the cloning of foreign sequences such as chimeric gene sequences containing a plant protox promoter.

EXAMPLE 6: Construction of Chimeric Genes/Plant Expression Cassettes

Coding sequences intended for expression in transgenic plants under the control of a plant protox promoter may be assembled in expression cassettes behind a suitable protox promoter and upstream of a suitable transcription terminator. The resulting chimeric genes can then be easily transferred to the plant transformation vectors described above in Example 19.

Protox Promoter Selection

In accordance with the present invention, the chimeric gene will contain a plant protox promoter. The selection of the specific protox promoter used in the chimeric gene is primarily up to the individual researcher, although generally it will be preferable to use a protox promoter from a plant species closely related to, or most preferably identical to, the species intended to contain the resulting chimeric gene. For example, if the chimeric gene is intended to be contained in a maize plant it would be preferable to use a protox promoter from a monocotyledenous plant and most preferable to use a maize protox promoter.

Transcriptional Terminators

A variety of transcriptional terminators are available for use in expression cassettes. These are responsible for the termination of transcription beyond the transgene and its correct polyadenylation. Appropriate transcriptional terminators are those which are known to function in plants and include the CaMV 35S terminator, the *tml* terminator, the nopaline synthase terminator, the pea *rbcS* E9 terminator, as well as terminators naturally associated with the plant protox gene (i.e. "protox terminators"). These can be used in both monocotyledons and dicotyledons.

Sequences for the Enhancement or Regulation of Expression

Numerous sequences have been found to enhance gene expression from within the transcriptional unit and these sequences can be used in conjunction with the genes of this invention to increase their expression in transgenic plants.

Various intron sequences have been shown to enhance expression, particularly in monocotyledonous cells. For example, the introns of the maize *Adh1* gene have been found to significantly enhance the expression of the wild-type gene under its cognate promoter when introduced into maize cells. Intron 1 was found to be particularly effective and enhanced expression in fusion constructs with the chloramphenicol acetyltransferase gene (Callis *et al.*, Genes Develop. *1*: 1183-1200 (1987)). In the same experimental system, the intron from the maize *bronze1* gene had a similar effect in enhancing expression (Callis *et al.*, *supra*). Intron sequences have been routinely incorporated into plant transformation vectors, typically within the non-translated leader.

A number of non-translated leader sequences derived from viruses are also known to enhance expression, and these are particularly effective in dicotyledonous cells. Specifically, leader sequences from Tobacco Mosaic Virus (TMV, the "W-sequence"), Maize Chlorotic Mottle Virus (MCMV), and Alfalfa Mosaic Virus (AMV) have been shown to be effective in enhancing expression (*e.g.* Gallie *et al. Nucl. Acids Res. 15*: 8693-8711 (1987); Skuzeski *et al. Plant Molec. Biol. 15*: 65-79 (1990))

Targeting of the Gene Product Within the Cell

Various mechanisms for targeting gene products are known to exist in plants and the sequences controlling the functioning of these mechanisms have been characterized in some detail. For example, the targeting of gene products to the chloroplast is controlled by a signal sequence found at the amino terminal end of various proteins and which is cleaved during chloroplast import yielding the mature protein (*e.g.* Comai *et al. J. Biol. Chem. 263*: 15104-15109 (1988)). These signal sequences can be fused to heterologous gene products to effect the import of heterologous products into the chloroplast (van den Broeck *et al. Nature 313*: 358-363 (1985)). DNA encoding for appropriate signal sequences can be isolated from the 5' end of the cDNAs

encoding the RUBISCO protein, the CAB protein, the EPSP synthase enzyme, the GS2 protein and many other proteins which are known to be chloroplast localized.

Other gene products are localized to other organelles such as the mitochondrion and the peroxisome (*e.g.* Unger *et al. Plant Molec. Biol. 13*: 411-418 (1989)). The cDNAs encoding these products can also be manipulated to effect the targeting of heterologous gene products to these organelles. Examples of such sequences are the nuclear-encoded ATPases and specific aspartate amino transferase isoforms for mitochondria. Targeting to cellular protein bodies has been described by Rogers *et al., Proc. Natl. Acad. Sci. USA 82*: 6512-6516 (1985)).

In addition sequences have been characterized which cause the targeting of gene products to other cell compartments. Amino terminal sequences are responsible for targeting to the ER, the apoplast, and extracellular secretion from aleurone cells (Koehler & Ho, *Plant Cell 2*: 769-783 (1990)). Additionally, amino terminal sequences in conjunction with carboxy terminal sequences are responsible for vacuolar targeting of gene products (Shinshi *et al., Plant Molec. Biol. 14*: 357-368 (1990)).

By the fusion of the appropriate targeting sequences described above to transgene sequences of interest it is possible to direct the transgene product to any organelle or cell compartment. For chloroplast targeting, for example, the chloroplast signal sequence from the RUBISCO gene, the CAB gene, the EPSP synthase gene, or the GS2 gene is fused in frame to the amino terminal ATG of the transgene. The signal sequence selected should include the known cleavage site and the fusion constructed should take into account any amino acids after the cleavage site which are required for cleavage. In some cases this requirement may be fulfilled by the addition of a small number of amino acids between the cleavage site and the transgene ATG or alternatively replacement of some amino acids within the transgene sequence. Fusions constructed for chloroplast import can be tested for efficacy of chloroplast uptake by *in vitro* translation of *in vitro* transcribed constructions followed by *in vitro* chloroplast uptake using techniques described by (Bartlett *et al.* In: Edelmann *et al.* (Eds.) Methods in Chloroplast Molecular Biology, Elsevier, pp 1081-1091 (1982); Wasmann *et al. Mol. Gen. Genet. 205*: 446-453 (1986)). These construction techniques are well known in the art and are equally applicable to mitochondria and peroxisomes. The choice of targeting which may be required for expression

of the transgenes will depend on the cellular localization of the precursor required as the starting point for a given pathway. This will usually be cytosolic or chloroplastic, although it may is some cases be mitochondrial or peroxisomal. The products of transgene expression will not normally require targeting to the ER, the apoplast or the vacuole.

The above described mechanisms for cellular targeting can be utilized in conjunction with plant protox promoters so as to effect a specific cell targeting goal under the transcriptional regulation of a promoter which has an expression pattern different to that of the promoter from which the targeting signal derives.

EXAMPLE 7: Transformation of Dicotyledons

Transformation techniques for dicotyledons are well known in the art and include *Agrobacterium*-based techniques and techniques which do not require *Agrobacterium*. Non-*Agrobacterium* techniques involve the uptake of exogenous genetic material directly by protoplasts or cells. This can be accomplished by PEG or electroporation mediated uptake, particle bombardment-mediated delivery, or microinjection. Examples of these techniques are described by Paszkowski *et al., EMBO J 3:* 2717-2722 (1984), Potrykus *et al., Mol. Gen. Genet. 199:* 169-177 (1985), Reich *et al., Biotechnology 4:* 1001-1004 (1986), and Klein *et al., Nature 327:* 70-73 (1987). In each case the transformed cells are regenerated to whole plants using standard techniques known in the art.

Agrobacterium-mediated transformation is a preferred technique for transformation of dicotyledons because of its high efficiency of transformation and its broad utility with many different species. The many crop species which are routinely transformable by *Agrobacterium* include tobacco, tomato, sunflower, cotton, oilseed rape, potato, soybean, alfalfa and poplar (EP 0 317 511 (cotton), EP 0 249 432 (tomato, to Calgene), WO 87/07299 (*Brassica*, to Calgene), US 4,795,855 (poplar)).

Transformation of the target plant species by recombinant *Agrobacterium* usually involves co-cultivation of the *Agrobacterium* with explants from the plant and follows protocols well known in the art. Transformed tissue is regenerated on selectable medium carrying the antibiotic or herbicide resistance marker present between the binary plasmid T-DNA borders.

EXAMPLE 8: Transformation of Monocotyledons

Transformation of most monocotyledon species has now also become routine. Preferred techniques include direct gene transfer into protoplasts using PEG or electroporation techniques, and particle bombardment into callus tissue. Transformations can be undertaken with a single DNA species or multiple DNA species (*i.e.* co-transformation) and both these techniques are suitable for use with this invention. Co-transformation may have the advantage of avoiding complex vector construction and of generating transgenic plants with unlinked loci for the gene of interest and the selectable marker, enabling the removal of the selectable marker in subsequent generations, should this be regarded desirable. However, a disadvantage of the use of co-transformation is the less than 100% frequency with which separate DNA species are integrated into the genome (Schocher *et al. Biotechnology 4:* 1093-1096 (1986)).

Patent Applications EP 0 292 435 (to Ciba-Geigy), EP 0 392 225 (to Ciba-Geigy), WO 93/07278 (to Ciba-Geigy) and U.S. Patent No. 5,350,689 (to Ciba-Geigy) describe techniques for the preparation of callus and protoplasts from an élite inbred line of maize, transformation of protoplasts using PEG or electroporation, and the regeneration of maize plants from transformed protoplasts. Gordon-Kamm *et al., Plant Cell 2:* 603-618 (1990)) and Fromm *et al., Biotechnology 8:* 833-839 (1990)) have published techniques for transformation of A188-derived maize line using particle bombardment. Furthermore, application WO 93/07278 (to Ciba-Geigy) and Koziel *et al., Biotechnology 11:* 194-200 (1993)) describe techniques for the transformation of élite inbred lines of maize by particle bombardment. This technique utilizes immature maize embryos of 1.5-2.5 mm length excised from a maize ear 14-15 days after pollination and a PDS-1000He Biolistics device for bombardment.

Transformation of rice can also be undertaken by direct gene transfer techniques utilizing protoplasts or particle bombardment. Protoplast-mediated transformation has been described for *Japonica*-types and *Indica*-types (Zhang *et al., Plant Cell Rep 7:* 379-384 (1988); Shimamoto *et al. Nature 338:* 274-277 (1989); Datta *et al. Biotechnology 8:* 735-740 (1990)). Both types are also routinely transformable using particle bombardment (Christou *et al. Biotechnology 9:* 957-962 (1991)).

Patent Application EP 0 332 581 (to Ciba-Geigy) describes techniques for the generation, transformation and regeneration of Pooideae protoplasts. These techniques allow the transformation of *Dactylis* and wheat. Furthermore, wheat transformation was been described by Vasil *et al.*, *Biotechnology 10*: 667-674 (1992)) using particle bombardment into cells of type C long-term regenerable callus, and also by Vasil *et al.*, *Biotechnology 11*: 1553-1558 (1993)) and Weeks *et al.*, *Plant Physiol. 102*: 1077-1084 (1993) using particle bombardment of immature embryos and immature embryo-derived callus. A preferred technique for wheat transformation, however, involves the transformation of wheat by particle bombardment of immature embryos and includes either a high sucrose or a high maltose step prior to gene delivery. Prior to bombardment, any number of embryos (0.75-1 mm in length) are plated onto MS medium with 3% sucrose (Murashige & Skoog, *Physiologia Plantarum 15*: 473-497 (1962)) and 3 mg/l 2,4-D for induction of somatic embryos which is allowed to proceed in the dark. On the chosen day of bombardment, embryos are removed from the induction medium and placed onto the osmoticum (*i.e.* induction medium with sucrose or maltose added at the desired concentration, typically 15%). The embryos are allowed to plasmolyze for 2-3 h and are then bombarded. Twenty embryos per target plate is typical, although not critical. An appropriate gene-carrying plasmid (such as pCIB3064 or pSG35) is precipitated onto micrometer size gold particles using standard procedures. Each plate of embryos is shot with the DuPont Biolistics• helium device using a burst pressure of ~1000 psi using a standard 80 mesh screen. After bombardment, the embryos are placed back into the dark to recover for about 24 h (still on osmoticum). After 24 hrs, the embryos are removed from the osmoticum and placed back onto induction medium where they stay for about a month before regeneration. Approximately one month later the embryo explants with developing embryogenic callus are transferred to regeneration medium (MS + 1 mg/liter NAA, 5 mg/liter GA), further containing the appropriate selection agent (10 mg/l basta in the case of pCIB3064 and 2 mg/l methotrexate in the case of pSOG35). After approximately one month, developed shoots are transferred to larger sterile containers known as "GA7s" which contained half-strength MS, 2% sucrose, and the same concentration of selection agent. Patent application 08/147,161 describes methods for wheat transformation and is hereby incorporated by reference.

* * * * * * * * * * * * *

While the present invention has been described with reference to specific embodiments thereof, it will be appreciated that numerous variations, modifications, and embodiments are possible, and accordingly, all such variations, modifications and embodiments are to be regarded as being within the spirit and scope of the present invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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Volrath, Sandra

(ii) TITLE OF INVENTION: PROMOTERS FROM PLANT PROTOPORPHYRINOGEN OXIDASE GENES

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:
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(C) CITY: Tarrytown
(D) STATE: NY
(E) COUNTRY: USA
(F) ZIP: 10591-9005

(v) COMPUTER READABLE FORM:
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(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

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(B) FILING DATE:
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(C) REFERENCE/DOCKET NUMBER: CGC 1846/prov2

(ix) TELECOMMUNICATION INFORMATION:
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(B) TELEFAX: 919-541-8689

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS.
(A) LENGTH: 1719 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 31..1644
(D) OTHER INFORMATION: /note= "Arabidopsis protox-1 cDNA: sequence from pNDC-2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Thr Thr Gln Ser Leu Leu Pro Ser Phe Ser Lys Pro Asn Leu Arg Leu
     10                  15                  20

AAT GTT TAT AAG CCT CTT AGA CTC CGT TGT TCA GTG GCC GGT GGA CCA       150
Asn Val Tyr Lys Pro Leu Arg Leu Arg Cys Ser Val Ala Gly Gly Pro
 25                  30                  35                  40

ACC GTC GGA TCT TCA AAA ATC GAA GGC GGA GGA GGC ACC ACC ATC ACG       198
Thr Val Gly Ser Ser Lys Ile Glu Gly Gly Gly Gly Thr Thr Ile Thr
                 45                  50                  55

ACG GAT TGT GTC ATT GTC GGC GGA GGT ATT AGT GGT CTT TGC ATC GCT       246
Thr Asp Cys Val Ile Val Gly Gly Gly Ile Ser Gly Leu Cys Ile Ala
             60                  65                  70

CAG GCG CTT GCT ACT AAG CAT CCT GAT GCT GCT CCG AAT TTA ATT GTG       294
Gln Ala Leu Ala Thr Lys His Pro Asp Ala Ala Pro Asn Leu Ile Val
         75                  80                  85

ACC GAG GCT AAG GAT CGT GTT GGA GGC AAC ATT ATC ACT CGT GAA GAG       342
Thr Glu Ala Lys Asp Arg Val Gly Gly Asn Ile Ile Thr Arg Glu Glu
     90                  95                 100

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105                 110                 115                 120

CCT GTG CTC ACT ATC GTG GTA GAT AGT GGT TTG AAG GAT GAT TTG GTG       438
Pro Met Leu Thr Met Val Val Asp Ser Gly Leu Lys Asp Asp Leu Val
                125                 130                 135

TTG GGA GAT CCT ACT GCG CCA AGG TTT GTG TTG TGG AAT GGG AAA TTG       486
Leu Gly Asp Pro Thr Ala Pro Arg Phe Val Leu Trp Asn Gly Lys Leu
            140                 145                 150

AGG CCG GTT CCA TCT AAG CTA ACA GAC TTA CCG TTC TTT GAT TTG ATG       534
Arg Pro Val Pro Ser Lys Leu Thr Asp Leu Pro Phe Phe Asp Leu Met
        155                 160                 165
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    170                 175                 180

CCG TCA CCT CCA GGT CGT GAA GAA TCT GTG GAG GAG TTT GTA CGG CGT     630
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185                 190                 195                 200

AAC CTC GGT GAT GAG GTT TTT GAC CGC CTG ATT GAA CCG TTT TGT TCA     678
Asn Leu Gly Asp Glu Val Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser
                205                 210                 215

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Gly Val Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala Ala Phe
            220                 225                 230

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    250                 255                 260

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265                 270                 275                 280

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                285                 290                 295

AAA GTT AAG TTG TCT TGG AAG CTC TCA GGT ATC ACT AAG CTG GAG AGC     966
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            300                 305                 310

GGA GGA TAC AAC TTA ACA TAT GAG ACT CCA GAT GGT TTA GTT TCC GTG    1014
Gly Gly Tyr Asn Leu Thr Tyr Glu Thr Pro Asp Gly Leu Val Ser Val
        315                 320                 325

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Gln Ser Lys Ser Val Val Met Thr Val Pro Ser His Val Ala Ser Gly
    330                 335                 340

CTC TTG CGC CCT CTT TCT GAA TCT GCT GCA AAT GCA CTC TCA AAA CTA    1110
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345                 350                 355                 360

TAT TAC CCA CCA GTT GCA GCA GTA TCT ATC TCG TAC CCG AAA GAA GCA    1158
Tyr Tyr Pro Pro Val Ala Ala Val Ser Ile Ser Tyr Pro Lys Glu Ala
                365                 370                 375

ATC CGA ACA GAA TGT TTG ATA GAT GGT GAA CTA AAG GGT TTT GGG CAA    1206
Ile Arg Thr Glu Cys Leu Ile Asp Gly Glu Leu Lys Gly Phe Gly Gln
            380                 385                 390

TTG CAT CCA CGC ACG CAA GGA GTT GAA ACA TTA GGA ACT ATC TAC AGC    1254
Leu His Pro Arg Thr Gln Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser
        395                 400                 405

TCC TCA CTC TTT CCA AAT CGC GCA CCG CCC GGA AGA ATT TTG CTG TTG    1302
Ser Ser Leu Phe Pro Asn Arg Ala Pro Pro Gly Arg Ile Leu Leu Leu
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      410                 415                 420

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425                 430                 435                 440

GCT GAG TTA GTG GAA GCA GTT GAC AGA GAT TTG AGG AAA ATG CTA ATT     1398
Gly Glu Leu Val Glu Ala Val Asp Arg Asp Leu Arg Lys Met Leu Ile
                445                 450                 455

AAG CCT AAT TCG ACC GAT CCA CTT AAA TTA GGA GTT AGG GTA TGG CCT     1446
Lys Pro Asn Ser Thr Asp Pro Leu Lys Leu Gly Val Arg Val Trp Pro
            460                 465                 470

CAA GCC ATT CCT CAG TTT CTA GTT GGT CAC TTT GAT ATC CTT GAC ACG     1494
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        475                 480                 485

GCT AAA TCA TCT CTA ACG TCT TCG GGC TAC GAA GGG CTA TTT TTG GGT     1542
Ala Lys Ser Ser Leu Thr Ser Ser Gly Tyr Glu Gly Leu Phe Leu Gly
    490                 495                 500

GGC AAT TAC GTC GCT GGT GTA GCC TTA GGC CGG TGT GTA GAA GGC GCA     1590
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505                 510                 515                 520

TAT GAA ACC GCG ATT GAG GTC AAC AAC TTC ATG TCA CGG TAC GCT TAC     1638
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Lys

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 537 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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 1               5                  10                  15

Phe Ser Lys Pro Asn Leu Arg Leu Asn Val Tyr Lys Pro Leu Arg Leu
            20                  25                  30

Arg Cys Ser Val Ala Gly Gly Pro Thr Val Gly Ser Ser Lys Ile Glu
        35                  40                  45

Gly Gly Gly Gly Thr Thr Ile Thr Thr Asp Cys Val Ile Val Gly Gly
    50                  55                  60

Gly Ile Ser Gly Leu Cys Ile Ala Gln Ala Leu Ala Thr Lys His Pro
65                  70                  75                  80
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Asp Ala Ala Pro Asn Leu Ile Val Thr Glu Ala Lys Asp Arg Val Gly
85 90 95

Gly Asn Ile Ile Thr Arg Glu Glu Asn Gly Phe Leu Trp Glu Glu Gly
100 105 110

Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr Met Val Val Asp
115 120 125

Ser Gly Leu Lys Asp Asp Leu Val Leu Gly Asp Pro Thr Ala Pro Arg
130 135 140

Phe Val Leu Trp Asn Gly Lys Leu Arg Pro Val Pro Ser Lys Leu Thr
145 150 155 160

Asp Leu Pro Phe Phe Asp Leu Met Ser Ile Gly Gly Lys Ile Arg Ala
165 170 175

Gly Phe Gly Ala Leu Gly Ile Arg Pro Ser Pro Pro Gly Arg Glu Glu
180 185 190

Ser Val Glu Glu Phe Val Arg Arg Asn Leu Gly Asp Glu Val Phe Glu
195 200 205

Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr Ala Gly Asp Pro Ser
210 215 220

Lys Leu Ser Met Lys Ala Ala Phe [illegible] Val Trp Lys Leu Glu Gln
225 230 235 240

Asn Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys Ala Ile Gln Glu Arg
245 250 255

Lys Asn Ala Pro Lys Ala Glu Arg Asp Pro Arg Leu Pro Lys Pro Gln
260 265 270

Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu Arg Met Leu Pro Glu
275 280 285

Ala Ile Ser Ala Arg Leu Gly Ser Lys Val Lys Leu Ser Trp Lys Leu
290 295 300

Ser Gly Ile Thr Lys Leu Glu Ser Gly Gly Tyr Asn Leu Thr Tyr Glu
305 310 315 320

Thr Pro Asp Gly Leu Val Ser Val Gln Ser Lys Ser Val Val Met Thr
325 330 335

Val Pro Ser His Val Ala Ser Gly Leu Leu Arg Pro Leu Ser Glu Ser
340 345 350

Ala Ala Asn Ala Leu Ser Lys Leu Tyr Tyr Pro Pro Val Ala Ala Val
355 360 365

Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg Thr Glu Cys Leu Ile Asp
370 375 380

Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln Gly Val
385 390 395 400

Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu Phe Pro Asn Arg Ala
405 410 415

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      Pro Gly Arg Ile Leu Leu Leu Asn Tyr Ile Gly Gly Ser Thr Asn
                  420                 425                 430

Thr Gly Ile Leu Ser Lys Ser Glu Gly Glu Leu Val Glu Ala Val Asp
            435                 440                 445

Arg Asp Leu Arg Lys Met Leu Ile Lys Pro Asn Ser Thr Asp Pro Leu
        450                 455                 460

Lys Leu Gly Val Arg Val Trp Pro Gln Ala Ile Pro Gln Phe Leu Val
465                 470                 475                 480

Gly His Phe Asp Ile Leu Asp Thr Ala Lys Ser Ser Leu Thr Ser Ser
                485                 490                 495

Gly Tyr Glu Gly Leu Phe Leu Gly Gly Asn Tyr Val Ala Gly Val Ala
            500                 505                 510

Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Thr Ala Ile Glu Val Asn
        515                 520                 525

Asn Phe Met Ser Arg Tyr Ala Tyr Lys
    530                 535
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1738 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 70..1596
(D) OTHER INFORMATION: /note= "Arabidopsis protox-2 cDNA: sequence from pNDC-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
TTTTTTACTT ATTTCCGTCA CTGCTTTCGA CTGGTCAGAG ATTTTGACTC TGAATTGTTG      60

CAGATAGCA ATG GCG TCT GGA GCA GTA GCA GAT CAT CAA ATT GAA GCG          108
          Met Ala Ser Gly Ala Val Ala Asp His Gln Ile Glu Ala
            1               5                  10

GTT TCA GGA AAA AGA GTC GCA GTC GTA GGT GCA GGT GTA AGT GGA CTT       156
Val Ser Gly Lys Arg Val Ala Val Val Gly Ala Gly Val Ser Gly Leu
        15                  20                  25

GCG GCG GCT TAC AAC TTG AAA TCG AGG GGT TTG AAT GTG ACT GTG TTT       204
Ala Ala Ala Tyr Lys Leu Lys Ser Arg Gly Leu Asn Val Thr Val Phe
    30                  35                  40                  45
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    \A GCT GAT GGA AGA GTA GGT GGG AAG TTG AGA AGT GTT ATG CAA AAT      252
     u Ala Asp Gly Arg Val Gly Gly Lys Leu Arg Ser Val Met Gln Asn
                   50                  55                  60

5   GGT TTG ATT TGG GAT GAA GGA GCA AAC ACC ATG ACT GAG GCT GAG CCA      300
    Gly Leu Ile Trp Asp Glu Gly Ala Asn Thr Met Thr Glu Ala Glu Pro
               65                  70                  75

    GAA GTT GGG AGT TTA CTT GAT GAT CTT GGG CTT CGT GAG AAA CAA CAA      348
10  Glu Val Gly Ser Leu Leu Asp Asp Leu Gly Leu Arg Glu Lys Gln Gln
           80                  85                  90

    TTT CCA ATT TCA CAG AAA AAG CGG TAT ATT GTG CGG AAT GGT GTA CCT      396
    Phe Pro Ile Ser Gln Lys Lys Arg Tyr Ile Val Arg Asn Gly Val Pro
15      95                 100                 105

    GTG ATG CTA CCT ACC AAT CCC ATA GAG CTG GTC ACA AGT AGT GTG CTC      444
    Val Met Leu Pro Thr Asn Pro Ile Glu Leu Val Thr Ser Ser Val Leu
110                 115                 120                 125

20  TCT ACC CAA TCT AAG TTT CAA ATC TTG TTG GAA CCA TTT TTA TGG AAG      492
    Ser Thr Gln Ser Lys Phe Gln Ile Leu Leu Glu Pro Phe Leu Trp Lys
                130                 135                 140

25  AAA AAG TCC TCA AAA GTC TCA GAT GCA TCT GCT GAA GAA AGT GTA AGC      540
    Lys Lys Ser Ser Lys Val Ser Asp Ala Ser Ala Glu Glu Ser Val Ser
            145                 150                 155

    GAG TTC TTT CAA CGC CAT TTT GGA CAA GAG GTT GTT GAC TAT CTC ATC      588
30  Glu Phe Phe Gln Arg His Phe Gly Gln Glu Val Val Asp Tyr Leu Ile
        160                 165                 170

    GAC CCT TTT GTT GGT GGA ACA AGT GCT GCG GAC CCT GAT TCC CTT TCA      636
    Asp Pro Phe Val Gly Gly Thr Ser Ala Ala Asp Pro Asp Ser Leu Ser
35  175                 180                 185

    ATG AAG CAT TCT TTC CCA GAT CTC TGG AAT GTA GAG AAA AGT TTT GGC      684
    Met Lys His Ser Phe Pro Asp Leu Trp Asn Val Glu Lys Ser Phe Gly
190                 195                 200                 205

40  TCT ATT ATA GTC GGT GCA ATC AGA ACA AAG TTT GCT GCT AAA GGT GGT      732
    Ser Ile Ile Val Gly Ala Ile Arg Thr Lys Phe Ala Ala Lys Gly Gly
                210                 215                 220

45  AAA AGT AGA GAC ACA AAG AGT TCT CCT GGC ACA AAA AAG GGT TCG CGT      780
    Lys Ser Arg Asp Thr Lys Ser Ser Pro Gly Thr Lys Lys Gly Ser Arg
            225                 230                 235

    GGG TCA TTC TCT TTT AAG GGG GGA ATC CAG ATT CTT CCT GAT ACC TTG      828
50  Gly Ser Phe Ser Phe Lys Gly Gly Met Gln Ile Leu Pro Asp Thr Leu
        240                 245                 250

    TGC AAA AGT CTC TCA CAT GAT GAG ATC AAT TTA GAC TCC AAG GTA CTC      876
    Cys Lys Ser Leu Ser His Asp Glu Ile Asn Leu Asp Ser Lys Val Leu
255                 260                 265

    TCT TTG TCT TAC AAT TCT GGA TCA AGA CAG GAG AAC TGG TCA TTA TCT      924
    Ser Leu Ser Tyr Asn Ser Gly Ser Arg Gln Glu Asn Trp Ser Leu Ser
270                 275                 280                 285

60  TGT GTT TCG CAT AAT GAA ACC CAG AGA CAA AAC CCC CAT TAT GAT GCT      972
    Cys Val Ser His Asn Glu Thr Gln Arg Gln Asn Pro His Tyr Asp Ala
                290                 295                 300
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     ATT ATG ACG GCT CCT CTG TGC AAT GTG AAG GAG ATG AAG GTT ATG          1020
Val Ile Met Thr Ala Pro Leu Cys Asn Val Lys Glu Met Lys Val Met
            305                 310                 315

AAA GGA GGA CAA CCC TTT CAG CTA AAC TTT CTC CCC GAG ATT AAT TAC          1068
Lys Gly Gly Gln Pro Phe Gln Leu Asn Phe Leu Pro Glu Ile Asn Tyr
        320                 325                 330

ATG CCC CTC TCG GTT TTA ATC ACC ACA TTC ACA AAG GAG AAA GTA AAG          1116
Met Pro Leu Ser Val Leu Ile Thr Thr Phe Thr Lys Glu Lys Val Lys
    335                 340                 345

AGA CCT CTT GAA GGC TTT GGG GTA CTC ATT CCA TCT AAG GAG CAA AAG          1164
Arg Pro Leu Glu Gly Phe Gly Val Leu Ile Pro Ser Lys Glu Gln Lys
350                 355                 360                 365

GAT GGT TTC AAA ACT CTA GGT ACA CTT TTT TCA TCA ATG ATG TTT CCA          1212
His Gly Phe Lys Thr Leu Gly Thr Leu Phe Ser Ser Met Met Phe Pro
                370                 375                 380

GAT CGT TCC CCT AGT GAC GTT CAT CTA TAT ACA ACT TTT ATT GGT GGG          1260
Asp Arg Ser Pro Ser Asp Val His Leu Tyr Thr Thr Phe Ile Gly Gly
            385                 390                 395

AGT AGG AAC CAG GAA CTA GCC AAA GCT TCC ACT GAC GAA TTA AAA CAA          1308
Ser Arg Asn Gln Glu Leu Ala Lys Ala Ser Thr Asp Glu Leu Lys Gln
        400                 405                 410

GTT GTG ACT TCT GAC CTT GAG CGA CTG TTG GGG GTT GAA GGT GAA CCC          1356
Val Val Thr Ser Asp Leu Glu Arg Leu Leu Gly Val Glu Gly Glu Pro
    415                 420                 425

GTG TCT GTC AAC CAT TAC TAT TGG AGG AAA GCA TTC CCG TTG TAT GAC          1404
Val Ser Val Asn His Tyr Tyr Trp Arg Lys Ala Phe Pro Leu Tyr Asp
430                 435                 440                 445

AGC AGC TAT GAC TCA GTC ATG GAA GCA ATT GAC AAG ATG GAG AAT GAT          1452
Ser Ser Tyr Asp Ser Val Met Glu Ala Ile Asp Lys Met Glu Asn Asp
            450                 455                 460

CTA CCT GGG TTC TTC TAT GCA GGT AAT CAT CGA GGG GGG CTC TCT GTT          1500
Leu Pro Gly Phe Phe Tyr Ala Gly Asn His Arg Gly Gly Leu Ser Val
        465                 470                 475

GGG AAA TCA ATA GCA TCA GGT TGC AAA GCA GCT GAC CTT GTG ATC TCA          1548
Gly Lys Ser Ile Ala Ser Gly Cys Lys Ala Ala Asp Leu Val Ile Ser
    480                 485                 490

TAC GTG GAG TCT TGC TCA AAT GAC AAG AAA CCA AAT GAC AGC TTA TAACATTGTC   1603
Tyr Leu Glu Ser Cys Ser Asn Asp Lys Lys Pro Asn Asp Ser Leu
495                 500                 505

AAGGTTCGTC CCTTTTTATC ACTTACTTTG TAAACTTGTA AAATGCAACA AGCCGCCGTG        1663

CGATTAGCCA ACAACTCAGC AAAACCCAGA TTCTCATAAG GCTCACTAAT TCCAGAATAA        1723

ACTATTTATG TAAAA                                                         1738
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 508 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Ser Gly Ala Val Ala Asp His Gln Ile Glu Ala Val Ser Gly
1 5 10 15

Lys Arg Val Ala Val Val Gly Ala Gly Val Ser Gly Leu Ala Ala Ala
20 25 30

Tyr Lys Leu Lys Ser Arg Gly Leu Asn Val Thr Val Phe Glu Ala Asp
35 40 45

Gly Arg Val Gly Gly Lys Leu Arg Ser Val Met Gln Asn Gly Leu Ile
50 55 60

Trp Asp Glu Gly Ala Asn Thr Met Thr Glu Ala Glu Pro Glu Val Gly
65 70 75 80

Ser Leu Leu Asp Asp Leu Gly Leu Arg Glu Lys Gln Gln Phe Pro Ile
85 90 95

Ser Gln Lys Lys Arg Tyr Ile Val Arg Asn Gly Val Pro Val Met Leu
100 105 110

Pro Thr Asn Pro Ile Glu Leu Val Thr Ser Ser Val Leu Ser Thr Gln
115 120 125

Ser Lys Phe Gln Ile Leu Leu Glu Pro Phe Leu Trp Lys Lys Lys Ser
130 135 140

Ser Lys Val Ser Asp Ala Ser Ala Glu Glu Ser Val Ser Glu Phe Phe
145 150 155 160

Gln Arg His Phe Gly Gln Glu Val Val Asp Tyr Leu Ile Asp Pro Phe
165 170 175

Val Gly Gly Thr Ser Ala Ala Asp Pro Asp Ser Leu Ser Met Lys His
180 185 190

Ser Phe Pro Asp Leu Trp Asn Val Glu Lys Ser Phe Gly Ser Ile Ile
195 200 205

Val Gly Ala Ile Arg Thr Lys Phe Ala Ala Lys Gly Gly Lys Ser Arg
210 215 220

Asp Thr Lys Ser Ser Pro Gly Thr Lys Lys Gly Ser Arg Gly Ser Phe
225 230 235 240

Ser Phe Lys Gly Gly Met Gln Ile Leu Pro Asp Thr Leu Cys Lys Ser
245 250 255

Leu Ser His Asp Glu Ile Asn Leu Asp Ser Lys Val Leu Ser Leu Ser
260 265 270

Tyr Asn Ser Gly Ser Arg Gln Glu Asn Trp Ser Leu Ser Cys Val Ser
275 280 285

His Asn Glu Thr Gln Arg Gln Asn Pro His Tyr Asp Ala Val Ile Met

290 295 300

Thr Ala Pro Leu Cys Asn Val Lys Glu Met Lys Val Met Lys Gly Gly
305 310 315 320

Gln Pro Phe Gln Leu Asn Phe Leu Pro Glu Ile Asn Tyr Met Pro Leu
325 330 335

Ser Val Leu Ile Thr Thr Phe Thr Lys Glu Lys Val Lys Arg Pro Leu
340 345 350

Glu Gly Phe Gly Val Leu Ile Pro Ser Lys Glu Gln Lys His Gly Phe
355 360 365

Lys Thr Leu Gly Thr Leu Phe Ser Ser Met Met Phe Pro Asp Arg Ser
370 375 380

Pro Ser Asp Val His Leu Tyr Thr Thr Phe Ile Gly Gly Ser Arg Asn
385 390 395 400

Gln Glu Leu Ala Lys Ala Ser Thr Asp Glu Leu Lys Gln Val Val Thr
405 410 415

Ser Asp Leu Gln Arg Leu Leu Gly Val Glu Gly Glu Pro Val Ser Val
420 425 430

Asn His Tyr Tyr Trp Arg Lys Ala Phe Pro Leu Tyr Asp Ser Ser Tyr
435 440 445

Asp Ser Val Met Glu Ala Ile Asp Lys Met Glu Asn Asp Leu Pro Gly
450 455 460

Phe Phe Tyr Ala Gly Asn His Arg Gly Gly Leu Ser Val Gly Lys Ser
465 470 475 480

Ile Ala Ser Gly Cys Lys Ala Ala Asp Leu Val Ile Ser Tyr Leu Glu
485 490 495

Ser Cys Ser Asn Asp Lys Lys Pro Asn Asp Ser Leu
500 505

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1691 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1443
(D) OTHER INFORMATION: /note= "Maize protox-1 cDNA (not full-length); sequence from pMDC-4; first seven nucleotides removed vs. first provisional"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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GCG GAC TGC GTC GTG GTG GGC GGA GGC ATC AGT GGC CTC TGC ACC GCG      48
Ala Asp Cys Val Val Val Gly Gly Gly Ile Ser Gly Leu Cys Thr Ala
 1               5                  10                  15

CAG GCG CTG GCC ACG CGG CAC GGC GTC GGG GAC GTG CTT GTC ACG GAG      96
Gln Ala Leu Ala Thr Arg His Gly Val Gly Asp Val Leu Val Thr Glu
            20                  25                  30

GCC CGC GCC CGC CCC GGC GGC AAC ATT ACC ACC GTG GAG CGC CCC GAG     144
Ala Arg Ala Arg Pro Gly Gly Asn Ile Thr Thr Val Glu Arg Pro Glu
        35                  40                  45

GAA GGG TAC CTC TGG GAG GAG GGT CCC AAC AGC TTC CAG CCC TCC GAC     192
Glu Gly Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp
    50                  55                  60

CCC GTT CTC ACC ATG GCC GTG GAC AGC GGA CTG AAG GAT GAC TTG GTT     240
Pro Val Leu Thr Met Ala Val Asp Ser Gly Leu Lys Asp Asp Leu Val
65                  70                  75                  80

TTT GGG GAC CCA AAC GCG CCG CGT TTC GTG CTG TGG GAG GGG AAG CTG     288
Phe Gly Asp Pro Asn Ala Pro Arg Phe Val Leu Trp Glu Gly Lys Leu
                85                  90                  95

AGG CCC GTG CCA TCC AAG CCC GCC GAC CTC CCG TTC TTC GAT CTC ATG     336
Arg Pro Val Pro Ser Lys Pro Ala Asp Leu Pro Phe Phe Asp Leu Met
            100                 105                 110

AGC ATC CCA GGG AAG CTC AGG GCC GGT CTA GGC GCG CTT GGC ATC CGC     384
Ser Ile Pro Gly Lys Leu Arg Ala Gly Leu Gly Ala Leu Gly Ile Arg
        115                 120                 125

CCG CCT CCT CCA GGC CGC GAA GAG TCA GTG GAG GAG TTC GTG CGC CGC     432
Pro Pro Pro Pro Gly Arg Glu Glu Ser Val Glu Glu Phe Val Arg Arg
    130                 135                 140

AAC CTC GGT GCT GAG GTC TTT GAG CGC CTC ATT GAG CCT TTC TGC TCA     480
Asn Leu Gly Ala Glu Val Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser
145                 150                 155                 160

GGT GTC TAT GCT GGT GAT CCT TCT AAG CTC AGC ATG AAG GCT GCA TTT     528
Gly Val Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala Ala Phe
                165                 170                 175

GGG AAG GTT TGG CGC TTG GAA GAA ACT GGA GGT AGT ATT ATT GGT GGA     576
Gly Lys Val Trp Arg Leu Glu Glu Thr Gly Gly Ser Ile Ile Gly Gly
            180                 185                 190

ACC ATC AAG ACA ATT CAG GAG AGG AGC AAG AAT CCA A.. ..A CCG AGG     624
Thr Ile Lys Thr Ile Gln Glu Arg Ser Lys Asn Pro Lys Pro Pro Arg
        195                 200                 205

GAT GCC CGC CTT CCG AAG CCA AAA GGG CAG ACA GTT GCA TCT TTC AGG     672
Asp Ala Arg Leu Pro Lys Pro Lys Gly Gln Thr Val Ala Ser Phe Arg
    210                 215                 220

AAG GGT CTT GCC ATG CTT CCA AAT GCC ATT ACA TCC AGC TTG GGT AGT     720
Lys Gly Leu Ala Met Leu Pro Asn Ala Ile Thr Ser Ser Leu Gly Ser
225                 230                 235                 240
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    AA  TC AAA CTA TCA TGG AAA CTC ACG AGC ATT ACA AAA TCA GAT GAC      768
    Lys Val Lys Leu Ser Trp Lys Leu Thr Ser Ile Thr Lys Ser Asp Asp
                245                 250                 255

    AAG GGA TAT GTT TTG GAG TAT GAA ACG CCA GAA GGG GTT GTT TCG GTG      816
    Lys Gly Tyr Val Leu Glu Tyr Glu Thr Pro Glu Gly Val Val Ser Val
            260                 265                 270

    CAG GCT AAA AGT GTT ATC ATG ACT ATT CCA TCA TAT GTT GCT AGC AAC      864
    Gln Ala Lys Ser Val Ile Met Thr Ile Pro Ser Tyr Val Ala Ser Asn
        275                 280                 285

    ATT TTG CGT CCA CTT TCA AGC GAT GCT GGA GAT GCT CTA TCA AGA TTC      912
    Ile Leu Arg Pro Leu Ser Ser Asp Ala Ala Asp Ala Leu Ser Arg Phe
    290                 295                 300

    TAT TAT CCA CCG GTT GCT GCT GTA ACT GTT TCG TAT CCA AAG GAA GCA      960
    Tyr Tyr Pro Pro Val Ala Ala Val Thr Val Ser Tyr Pro Lys Glu Ala
305                 310                 315                 320

    ATT AGA AAA GAA TGC TTA ATT GAT GGG CAA CTC CAG GGC TTT GGC CAG     1008
    Ile Arg Lys Glu Cys Leu Ile Asp Gly Glu Leu Gln Gly Phe Gly Gln
                325                 330                 335

    TTC GAT CCA CGT AGT CAA GGA GTT GAG ACA TTA GGA ACA ATA TAC AGT     1056
    Leu His Pro Arg Ser Gln Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser
            340                 345                 350

    TCC TCA CTC TTT CCA AAT CGT GCT CCT GAC GGT AGG GTC TTA CTT CTA     1104
    Ser Ser Leu Phe Pro Asn Arg Ala Pro Asp Gly Arg Val Leu Leu Leu
        355                 360                 365

    AAC TAC ATA GGA GGT GCT ACA AAC ACA GGA ATT GTT TCC AAG ACT GAA     1152
    Asn Tyr Ile Gly Gly Ala Thr Asn Thr Gly Ile Val Ser Lys Thr Glu
    370                 375                 380

    AGT GAG CTG GTC GAA GCA GTT GAC CGT GAC CTC CGA AAA ATG CTT ATA     1200
    Ser Glu Leu Val Glu Ala Val Asp Arg Asp Leu Arg Lys Met Leu Ile
385                 390                 395                 400

    AAT TCT ACA GCA GTG GAC CCT TTA GTC CTT GGT GTT CGA GTT TGG CCA     1248
    Asn Ser Thr Ala Val Asp Pro Leu Val Leu Gly Val Arg Val Trp Pro
                405                 410                 415

    CAA GCC ATA GCT CAC TTC CTG GTA GGA CAT CTT GAT CTT CTG GAA GCC     1296
    Gln Ala Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu Glu Ala
            420                 425                 430

    GCA AAA GCT GCC CTG GAC CGA GGT GGC TAC GAT GGG CTG TTC CTA GGA     1344
    Ala Lys Ala Ala Leu Asp Arg Gly Gly Tyr Asp Gly Leu Phe Leu Gly
        435                 440                 445

    GGG AAC TAT GTT GCA GGA GTT GCC CTG GGC AGA TGC GTT GAC GGC GCG     1392
    Gly Asn Tyr Val Ala Gly Val Ala Leu Gly Arg Cys Val Glu Gly Ala
    450                 455                 460

    TAT GAA AGT GCC TCG CAA ATA TCT GAC TTC TTG ACC AAG TAT GCC TAC     1440
    Tyr Glu Ser Ala Ser Gln Ile Ser Asp Phe Leu Thr Lys Tyr Ala Tyr
465                 470                 475                 480

    AAG TGATGAAAGA AGTGGAGCGC TACTTGTTAA TCGTTTATGT TGCATAGATG        1493
    Lys

                                35
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GTCCCTCC CGGGAAAAAA AAGCTTGAAT AGTATTTTTT ATTCTTATTT TGTAAATTGC 1553

ATTTCTGTTC TTTTTTCTAT CAGTAATTAG TTATATTTTA GTTCTGTAGG AGATTGTTCT 1613

GTTCACTCCC CTTCAAAAGA AATTTTATTT TTCATTCTTT TATGAGAGCT GTGCTACTTA 1673

AAAAAAAAAA AAAAAAAA 1691

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 481 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Asp Cys Val Val Val Gly Gly Gly Ile Ser Gly Leu Cys Thr Ala
1 5 10 15

Gln Ala Leu Ala Thr Arg His Gly Val Gly Asp Val Leu Val Thr Glu
20 25 30

Ala Arg Ala Arg Pro Gly Gly Asn Ile Thr Thr Val Glu Arg Pro Glu
35 40 45

Glu Gly Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp
50 55 60

Pro Val Leu Thr Met Ala Val Asp Ser Gly Leu Lys Asp Asp Leu Val
65 70 75 80

Phe Gly Asp Pro Asn Ala Pro Arg Phe Val Leu Trp Glu Gly Lys Leu
85 90 95

Arg Pro Val Pro Ser Lys Pro Ala Asp Leu Pro Phe Phe Asp Leu Met
100 105 110

Ser Ile Pro Gly Lys Leu Arg Ala Gly Leu Gly Ala Leu Gly Ile Arg
115 120 125

Pro Pro Pro Pro Gly Arg Glu Glu Ser Val Glu Glu Phe Val Arg Arg
130 135 140

Asn Leu Gly Ala Glu Val Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser
145 150 155 160

Gly Val Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala Ala Phe
165 170 175

Gly Lys Val Trp Arg Leu Glu Glu Thr Gly Gly Ser Ile Ile Gly Gly
180 185 190

Thr Ile Lys Thr Ile Gln Glu Arg Ser Lys Asn Pro Lys Pro Pro Arg
195 200 205

Asp Ala Arg Leu Pro Lys Pro Lys Gly Gln Thr Val Ala Ser Phe Arg
210 215 220

Lys Gly Leu Ala Met Leu Pro Asn Ala Ile Thr Ser Ser Leu Gly Ser
230 235 240

Lys Val Lys Leu Ser Trp Lys Leu Thr Ser Ile Thr Lys Ser Asp Asp
245 250 255

Lys Gly Tyr Val Leu Glu Tyr Glu Thr Pro Glu Gly Val Val Ser Val
260 265 270

Gln Ala Lys Ser Val Ile Met Thr Ile Pro Ser Tyr Val Ala Ser Asn
275 280 285

Ile Leu Arg Pro Leu Ser Ser Asp Ala Ala Asp Ala Leu Ser Arg Phe
290 295 300

Tyr Tyr Pro Pro Val Ala Ala Val Thr Val Ser Tyr Pro Lys Glu Ala
305 310 315 320

Ile Arg Lys Glu Cys Leu Ile Asp Gly Glu Leu Gln Gly Phe Gly Gln
325 330 335

Leu His Pro Arg Ser Gln Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser
340 345 350

Ser Ser Leu Phe Pro Asn Arg Ala Pro Asp Gly Arg Val Leu Leu Leu
355 360 365

Asn Tyr Ile Gly Gly Ala Thr Asn Thr Gly Ile Val Ser Lys Thr Glu
370 375 380

Ser Glu Leu Val Glu Ala Val Asp Arg Asp Leu Arg Lys Met Leu Ile
385 390 395 400

Asn Ser Thr Ala Val Asp Pro Leu Val Leu Gly Val Arg Val Trp Pro
405 410 415

Gln Ala Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu Glu Ala
420 425 430

Ala Lys Ala Ala Leu Asp Arg Gly Gly Tyr Asp Gly Leu Phe Leu Gly
435 440 445

Gly Asn Tyr Val Ala Gly Val Ala Leu Gly Arg Cys Val Glu Gly Ala
450 455 460

Tyr Glu Ser Ala Ser Gln Ile Ser Asp Phe Leu Thr Lys Tyr Ala Tyr
465 470 475 480

Lys

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2061 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 64..1698
(D) OTHER INFORMATION: /note= "Maize protox-2 cDNA; sequence from pMDC-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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GTCTCCTACC TCCACCTCCA CGACAACAAG CAAATCCCCA TCCAGTTCCA AACCCTAACT      60

CAA ATG CTC GCT TTG ACT GCC TCA GCC TCA TCC GCT TCG TCC GAT CCT      108
    Met Leu Ala Leu Thr Ala Ser Ala Ser Ser Ala Ser Ser His Pro
     1               5                  10                  15

TAT CGC CAC GCC TCC GCG CAC ACT CGT CGC CCC CGC CTA CGT GCG GTC      156
Tyr Arg His Ala Ser Ala His Thr Arg Arg Pro Arg Leu Arg Ala Val
            20                  25                  30

CTC GCG ATG GCG GGC TCC GAC GAC CCC CGT GCA GCG CCC GCC AGA TCG      204
Leu Ala Met Ala Gly Ser Asp Asp Pro Arg Ala Ala Pro Ala Arg Ser
        35                  40                  45

GTC GCC GTC GTC GGC GCC GGG GTC AGC GGG CTC GCG GCG GCG TAC AGG      252
Val Ala Val Val Gly Ala Gly Val Ser Gly Leu Ala Ala Ala Tyr Arg
    50                  55                  60

CTC AGA CAG AGC GGC GTG AAC GTA ACG GTG TTC GAA GCG GCC GAC AGG      300
Leu Arg Gln Ser Gly Val Asn Val Thr Val Phe Glu Ala Ala Asp Arg
65                  70                  75

GCG GGA GGA AAG ATA CGG ACC AAT TCC GAG GGC GGG TTT GTC TGG GAT      348
Ala Gly Gly Lys Ile Arg Thr Asn Ser Glu Gly Gly Phe Val Trp Asp
 80                  85                  90                  95

GAA GGA GCT AAC ACC ATG ACA GAA GGT GAA TGG GAG GCC AGT AGA CTG      396
Glu Gly Ala Asn Thr Met Thr Glu Gly Glu Trp Glu Ala Ser Arg Leu
            100                 105                 110

ATT GAT GAT CTT GGT CTA CAA GAC AAA CAG CAC TAT CCT AAC TCC CAA      444
Ile Asp Asp Leu Gly Leu Gln Asp Lys Gln Gln Tyr Pro Asn Ser Gln
        115                 120                 125

CAC AAG CGT TAC ATT GTC AAA GAT GGA GCA CCA GCA CTG ATT CCT TCG      492
His Lys Arg Tyr Ile Val Lys Asp Gly Ala Pro Ala Leu Ile Pro Ser
    130                 135                 140

GAT CCC ATT TCG CTA ATG AAA AGC AGT GTT CTT TCG ACA AAA TCA AAG      540
Asp Pro Ile Ser Leu Met Lys Ser Ser Val Leu Ser Thr Lys Ser Lys
145                 150                 155

ATT GCG TTA TTT TTT GAA CCA TTT CTC TAC AAG AAA GCT AAC ACA AGA      588
Ile Ala Leu Phe Phe Glu Pro Phe Leu Tyr Lys Lys Ala Asn Thr Arg
160                 165                 170                 175

AAC TCT GGA AAA GTG TCT GAG GAC CAC TTG AGT GAG AGT GTT CGG AGC      636
Asn Ser Gly Lys Val Ser Glu Glu His Leu Ser Glu Ser Val Gly Ser
            180                 185                 190
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     T   TGT GAA CGC CAC TTT GGA AGA GAA GTT GTT GAC TAT TTT GTT GAT          684
     P.  Cys Glu Arg His Phe Gly Arg Glu Val Val Asp Tyr Phe Val Asp
                 195                 200                 205

5    CCA TTT GTA GCT GGA ACA AGT GCA GGA GAT CCA GAG TCA CTA TCT ATT          732
     Pro Phe Val Ala Gly Thr Ser Ala Gly Asp Pro Glu Ser Leu Ser Ile
             210                 215                 220

10   CGT CAT GCA TTC CCA GCA TTG TGG AAT TTG GAA AGA AAG TAT GGT TCA          780
     Arg His Ala Phe Pro Ala Leu Trp Asn Leu Glu Arg Lys Tyr Gly Ser
     225                 230                 235

15   GTT ATT GTT GGT GCC ATC TTG TCT AAG CTA GCA GGT AAA GCT GAT CCA          828
     Val Ile Val Gly Ala Ile Leu Ser Lys Leu Ala Ala Lys Gly Asp Pro
     240                 245                 250                 255

     GTA AAG ACA AGA CAT GAT TCA TCA GGG AAA AGA AGG AAT AGA CGA GTG          876
20   Val Lys Thr Arg His Asp Ser Ser Gly Lys Arg Arg Asn Arg Arg Val
                 260                 265                 270

     TCG TTT TCA TTT CAT GGT GGA ATG CAG TCA CTA ATA AAT GCA CTT CAC          924
     Ser Phe Ser Phe His Gly Gly Met Gln Ser Leu Ile Asn Ala Leu His
25           275                 280                 285

     AAT GAA GTT GGA GAT GAT AAT GTG AAG CTT GGT ACA GAA GTG TTG TCA          972
     Asn Glu Val Gly Asp Asp Asn Val Lys Leu Gly Thr Glu Val Leu Ser
             290                 295                 300

30   TTG GCA TGT ACA TTT GAT GGA GTT CCT GCA CTA GGC AGG TGG TCA ATT         1020
     Leu Ala Cys Thr Phe Asp Gly Val Pro Ala Leu Gly Arg Trp Ser Ile
     305                 310                 315

     TCT GTT GAT TCG AAG GAT AGC GGT GAC AAG GAC CTT GCT AGT AAC CAA         1068
35   Ser Val Asp Ser Lys Asp Ser Gly Asp Lys Asp Leu Ala Ser Asn Gln
     320                 325                 330                 335

     ACC TTT GAT GCT GTT ATA ATG ACA GCT CCA TTG TCA AAT GTC GGG AGG         1116
     Thr Phe Asp Ala Val Ile Met Thr Ala Pro Leu Ser Asn Val Arg Arg
40           340                 345                 350

     ATG AAG TTC ACC AAA GGT GGA GCT CCG GTT GTT CTT GAC TTT CTT CCT         1164
     Met Lys Phe Thr Lys Gly Gly Ala Pro Val Val Leu Asp Phe Leu Pro
45           355                 360                 365

     AAG ATG GAT TAT CTA CCA CTA TCT GTC ATG GTG ACT GCT TTT AAG AAG         1212
     Lys Met Asp Tyr Leu Pro Leu Ser Leu Met Val Thr Ala Phe Lys Lys
             370                 375                 380

50   GAT GAT GTC AAG AAA CCT CTG GAA GGA TTT GGG GTC TTA ATA CCT TAC         1260
     Asp Asp Val Lys Lys Pro Leu Glu Gly Phe Gly Val Leu Ile Pro Tyr
     385                 390                 395

     AAG GAA CAG CAA AAA CAT GGT CTG AAA ACC CTT GGG ACT CTC TTT TCC         1308
55   Lys Glu Gln Gln Lys His Gly Leu Lys Thr Leu Gly Thr Leu Phe Ser
     400                 405                 410                 415

     TCA ATG ATG TTC CCA GAT CGA GCT CCT GAT GAC CAA TAT TTA TAT ACA         1356
     Ser Met Met Phe Pro Asp Arg Ala Pro Asp Asp Gln Tyr Leu Tyr Thr
60           420                 425                 430

     ACA TTT GTT GGG GGT AGC CAC AAT AGA GAT CTT GCT CCA GCT CCA ACG         1404
     Thr Phe Val Gly Gly Ser His Asn Arg Asp Leu Ala Gly Ala Pro Thr
                                 39
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                435                 440                 445

TCT ATT CTG AAA CAA CTT GTG ACC TCT GAC CTT AAA AAA CTC TTG GGC      1452
Ser Ile Leu Lys Gln Leu Val Thr Ser Asp Leu Lys Lys Leu Leu Gly
    450                 455                 460

GTA GAG GGG CAA CCA ACT TTT GTC AAG CAT GTA TAC TGG GGA AAT GCT      1500
Val Glu Gly Gln Pro Thr Phe Val Lys His Val Tyr Trp Gly Asn Ala
465                 470                 475

TTT CCT TTG TAT GGC CAT GAT TAT AGT TCT GTA TTG GAA GCT ATA GAA      1548
Phe Pro Leu Tyr Gly His Asp Tyr Ser Ser Val Leu Glu Ala Ile Glu
480                 485                 490                 495

AAG ATG GAG AAA AAC CTT CCA GGG TTC TTC TAC GCA GGA AAT AGC AAG      1596
Lys Met Glu Lys Asn Leu Pro Gly Phe Phe Tyr Ala Gly Asn Ser Lys
                500                 505                 510

GAT GGG CTT GCT GTT GGA AGT GTT ATA GCT TCA GGA AGC AAG GCT GCT      1644
Asp Gly Leu Ala Val Gly Ser Val Ile Ala Ser Gly Ser Lys Ala Ala
            515                 520                 525

GAC CTT GCA ATC TCA TAT CTT GAA TCT CAC ACC AAG CAT AAT AAT TCA      1692
Asp Leu Ala Ile Ser Tyr Leu Glu Ser His Thr Lys His Asn Asn Ser
        530                 535                 540

CAT TGAAAGTGTC TGACCTATCC TCTAGCAGTT GTGGACAAAT TTCTCCAGTT           1745
His
    545

CATGTACAGT AGAAACCGAT GCGTTGCAGT TTCAGAACAT CTTCACTTCT TCAGATATTA    1805

ACCCTTCGTT GAACATCCAC CAGAAAGGTA GTCACATGTG TAAGTGGGAA AATGAGGTTA    1865

AAAACTATTA TGGCGGCCGA AATGTTCCTT TTTGTTTTCC TCACAAGTGG CCTACGACAC    1925

TTGATGTTGG AAATACATTT AAATTTGTTG AATTGTTTGA GAACACATGC GTGACGTGTA    1985

ATATTTGCCT ATTGTGATTT TAGCAGTAGT CTTGGCCAGA TTATGCTTTA CGCCTTTAAA    2045

AAAAAAAAAA AAAAAA                                                    2061
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(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1811 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 3..1589
(D) OTHER INFORMATION: /product= "wheat protox-1 cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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                                                                        47
    TC GCA ACA ATG GCC ACC GCC ACC GTC GCG GCC GCG TCG CCG CTC CGC
       Ala Thr Met Ala Thr Ala Thr Val Ala Ala Ala Ser Pro Leu Arg
         1               5                  10                  15

                                                                        95
    GGC AGG GTC ACC GGG CGC CCA CAC CGC GTC CGC CCG CGT TGC GCT ACC
    Gly Arg Val Thr Gly Arg Pro His Arg Val Arg Pro Arg Cys Ala Thr
                    20                  25                  30

                                                                       143
    GCG AGC AGC TCG ACC GAG ACT CCG GCG GCG CCC GGC GTG CGG CTG TCC
    Ala Ser Ser Ala Thr Glu Thr Pro Ala Ala Pro Gly Val Arg Leu Ser
                35                  40                  45

                                                                       191
    GCG GAA TGC GTC ATT GTG GGC GCC GGG ATC AGC GGC CTC TGC ACC GCC
    Ala Glu Cys Val Ile Val Gly Ala Gly Ile Ser Gly Leu Cys Thr Ala
            50                  55                  60

                                                                       239
    CAG GCG CTG GCC ACC CGA TAC GGC GTC AGC GAC CTG CTC GTC ACG GAG
    Gln Ala Leu Ala Thr Arg Tyr Gly Val Ser Asp Leu Leu Val Thr Glu
        65                  70                  75

                                                                       287
    GCC CGC GAC CGC CCG GGC GGC AAC ATC ACC ACC GTC GAG CGT CCC GAC
    Ala Arg Asp Arg Pro Gly Gly Asn Ile Thr Thr Val Glu Arg Pro Asp
    80                  85                  90                  95

                                                                       335
    GAG GGG TAC CTG TGG GAG GAG GCA CCC AAC AGC TTC CAG CCC TCC GAC
    Glu Gly Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp
                100                 105                 110

                                                                       383
    CCG GTC CTC ACC ATG GCC GTG GAC AGC GGG CTC AAG GAT GAC TTG GTC
    Pro Val Leu Thr Met Ala Val Asp Ser Gly Leu Lys Asp Asp Leu Val
            115                 120                 125

                                                                       431
    TTC GGG GAC CCC AAC GCC CCC CGG TTC GTG CTC TGG GAG GGG AAG CTG
    Phe Gly Asp Pro Asn Ala Pro Arg Phe Val Leu Trp Glu Gly Lys Leu
        130                 135                 140

                                                                       479
    AGG CCG GTG CCG TCG AAG CCA GGC GAC CTG CCT TTC TTC AGC CTC ATG
    Arg Pro Val Pro Ser Lys Pro Gly Asp Leu Pro Phe Phe Ser Leu Met
    145                 150                 155

                                                                       527
    AGT ATC CCT GGG AAG CTC AGG GCC GGC CTT GGC GCG CTC GGC ATT CGC
    Ser Ile Pro Gly Lys Leu Arg Ala Gly Leu Gly Ala Leu Gly Ile Arg
160                 165                 170                 175

                                                                       575
    CCA CCT CCT CCA GGG CGC GAG GAG TCG GTG GAG GAG TTT GTG CGC CGC
    Pro Pro Pro Pro Gly Arg Glu Glu Ser Val Glu Glu Phe Val Arg Arg
                180                 185                 190

                                                                       623
    AAC CTC GGT GCC GAG GTC TTT GAG CGC CTC ATC GAG CCT TTC TGC TCA
    Asn Leu Gly Ala Glu Val Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser
            195                 200                 205

                                                                       671
    GGT GTA TAT GCT GGT GAT CCT TCG AAG CTT ACT ATG AAG GGT GCA TTT
    Gly Val Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala Ala Phe
        210                 215                 220

                                                                       719
    GGG AAG GTC TGG AGG TTG GAG GAG ATT GGA GGT AGT ATT ATT GGT GGA
    Gly Lys Val Trp Arg Leu Glu Glu Ile Gly Gly Ser Ile Ile Gly Gly
    225                 230                 235

                                                                       767
    ACC ATC AAG GCG ATT CAG GAT AAA GGG AAC AAC CCC AAA CCG CCA AGG
    Thr Ile Lys Ala Ile Gln Asp Lys Gly Lys Asn Pro Lys Pro Pro Arg
                                41
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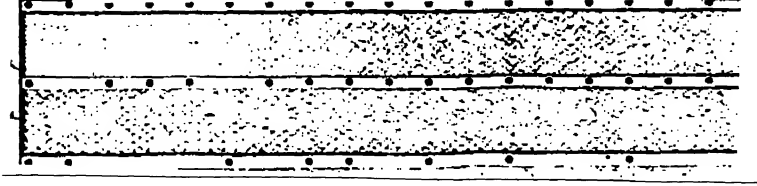

240 245 250 255

AT CCC CGA CTT CCG GCA CCA AAG GGA CAC ACG GTG GCA TCT TTC AGG 815
Asp Pro Arg Leu Pro Ala Pro Lys Gly Gln Thr Val Ala Ser Phe Arg
260 265 270

AAG GGT CTA GCC ATG CTC CCG AAT GCC ATC GCA TCT AGG CTG GGT AGT 863
Lys Gly Leu Ala Met Leu Pro Asn Ala Ile Ala Ser Arg Leu Gly Ser
275 280 285

AAA GTC AAG CTG TCA TGG AAG CTT ACC AGC ATT ACA AAG GCG GAC AAC 911
Lys Val Lys Leu Ser Trp Lys Leu Thr Ser Ile Thr Lys Ala Asp Asn
290 295 300

CAA GGA TAT GTA TTA GGT TAT GAA ACA CCA GAA GGA CTT GTT TCA GTG 959
Gln Gly Tyr Val Leu Gly Tyr Glu Thr Pro Glu Gly Leu Val Ser Val
305 310 315

CAG GCT AAA AGT GTT ATC ATG ACC ATC CCG TCA TAT GTT GCT AGT GAT 1007
Gln Ala Lys Ser Val Ile Met Thr Ile Pro Ser Tyr Val Ala Ser Asp
320 325 330 335

ATC TTG CGC CCA CTT TCA ATT GAT GCA GCA GAT GCA CTC TCA AAA TTC 1055
Ile Leu Arg Pro Leu Ser Ile Asp Ala Ala Asp Ala Leu Ser Lys Phe
340 345 350

TAT TAT CCG CCA GTT GCT GCT GTA ACT GTT TCA TAT CCA AAA GAA GCT 1103
Tyr Tyr Pro Pro Val Ala Ala Val Thr Val Ser Tyr Pro Lys Glu Ala
355 360 365

ATT AGA AAA GAA TGC TTA ATT GAT GGG GAG CTC CAG GGT TTC GGC CAG 1151
Ile Arg Lys Glu Cys Leu Ile Asp Gly Glu Leu Gln Gly Phe Gly Gln
370 375 380

TTG CAT CCA CCT AGC CAA GGA GTC GAG ACT TTA GGG ACA ATA TAT AGC 1199
Leu His Pro Arg Ser Gln Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser
385 390 395

TCT TCT CTC TTT CCT AAT CGT GCT CCT GCT GGA AGA GTG TTA CTT CTG 1247
Ser Ser Leu Phe Pro Asn Arg Ala Pro Ala Gly Arg Val Leu Leu Leu
400 405 410 415

AAC TAT ATC GGC ATT TCT ACA AAT ACA GGG ATC GTC TCC AAG ACT GAG 1295
Asn Tyr Ile Gly Gly Ser Thr Asn Thr Gly Ile Val Ser Lys Thr Glu
420 425 430

AGT GAC TTA GTA GGA GCC GTT GAC CGT GAC GTC AGA AAA ATG TTG ATA 1343
Ser Asp Leu Val Gly Ala Val Asp Arg Asp Leu Arg Lys Met Leu Ile
435 440 445

AAC CCT AGA GCA GCA GAC CCT TTA GCA TTA GGG GTT CGA GTC TGG CCA 1391
Asn Pro Arg Ala Ala Asp Pro Leu Ala Leu Gly Val Arg Val Trp Pro
450 455 460

CAA GCA ATA CCA CAG TTT TTG ATT GTG CAC CTT GAT CGC CTT GCT GCT 1439
Gln Ala Ile Pro Gln Phe Leu Ile Gly His Leu Asp Arg Leu Ala Ala
465 470 475

GCA AAA TCT GCA CTG GGC CAA GGC GGC TAC GAC GGG TTG TTC CTA GTA 1487
Ala Lys Ser Ala Leu Gly Gln Gly Gly Tyr Asp Gly Leu Phe Leu Gly
480 485 490 495

GGA AAC TAC GTC GCA GGA GTT GCC TTG GGC CGA TGC ATC GAG GGT GCG 1535

```
Gly Asn Tyr Val Ala Gly Val Ala Leu Gly Arg Cys Ile Glu Gly Ala
                500                 505                 510

AAC GAG AGT GCC TCA CAA GTA TCT GAC TTC TTG ACC AAG TAT GCC TAC      1583
Tyr Glu Ser Ala Ser Gln Val Ser Asp Phe Leu Thr Lys Tyr Ala Tyr
        515                 520                 525

AAG TGA TGGAAGTAGT GCATCTCTTC ATTTTGTTGC ATATACGAGG TGAGGCTAGG       1639
Lys *

ATCGGTAAAA CATCATGAGA TTCTGTAGTG TTTCTTTAAT TGAAAAAACA AATTTTAGTG    1699

ATGCAATATC TGCTCTTTCC TGTAGTTCCA GCATGTACAT CGGTATGGGA TAAAGTAGAA    1759

TAAGCTATTC TGCAAAAGCA GTGATTTTTT TTGAAAAAAA AAAAAAAAAA AA             1811


(2) INFORMATION FOR SEQ ID NO:10:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 529 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: protein

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Thr Met Ala Thr Ala Thr Val Ala Ala Ala Ser Pro Leu Arg Gly
 1               5                  10                  15

Arg Val Thr Gly Arg Pro His Arg Val Arg Pro Arg Cys Ala Thr Ala
            20                  25                  30

Ser Ser Ala Thr Glu Thr Pro Ala Ala Pro Gly Val Arg Leu Ser Ala
        35                  40                  45

Glu Cys Val Ile Val Gly Ala Gly Ile Ser Gly Leu Cys Thr Ala Gln
    50                  55                  60

Ala Leu Ala Thr Arg Tyr Gly Val Ser Asp Leu Leu Val Thr Glu Ala
65                  70                  75                  80

Arg Asp Arg Pro Gly Gly Asn Ile Thr Thr Val Glu Arg Pro Asp Glu
                85                  90                  95

Gly Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro
            100                 105                 110

Val Leu Thr Met Ala Val Asp Ser Gly Leu Lys Asp Asp Leu Val Phe
        115                 120                 125

Gly Asp Pro Asn Ala Pro Arg Phe Val Leu Trp Glu Gly Lys Leu Arg
    130                 135                 140

Pro Val Pro Ser Lys Pro Gly Asp Leu Pro Phe Phe Ser Leu Met Ser
145                 150                 155                 160

Ile Pro Gly Lys Leu Arg Ala Gly Leu Gly Ala Leu Gly Ile Arg Pro
                165                 170                 175

Pro Pro Pro Gly Arg Glu Glu Ser Val Glu Glu Phe Val Arg Arg Asn
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180 185 190

Leu Gly Ala Glu Val Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly
195 200 205

Val Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly
210 215 220

Lys Val Trp Arg Leu Glu Glu Ile Gly Gly Ser Ile Ile Gly Gly Thr
225 230 235 240

Ile Lys Ala Ile Gln Asp Lys Gly Lys Asn Pro Lys Pro Pro Arg Asp
245 250 255

Pro Arg Leu Pro Ala Pro Lys Gly Gln Thr Val Ala Ser Phe Arg Lys
260 265 270

Gly Leu Ala Met Leu Pro Asn Ala Ile Ala Ser Arg Leu Gly Ser Lys
275 280 285

Val Lys Leu Ser Trp Lys Leu Thr Ser Ile Thr Lys Ala Asp Asn Gln
290 295 300

Gly Tyr Val Leu Gly Tyr Glu Thr Pro Glu Gly Leu Val Ser Val Gln
305 310 315 320

Ala Lys Ser Val Ile Met Thr Ile Pro Ser Tyr Val Ala Ser Asp Ile
325 330 335

Leu Arg Pro Leu Ser Ile Asp Ala Ala Asp Ala Leu Ser Lys Phe Tyr
340 345 350

Tyr Pro Pro Val Ala Ala Val Thr Val Ser Tyr Pro Lys Glu Ala Ile
355 360 365

Arg Lys Glu Cys Leu Ile Asp Gly Glu Leu Gln Gly Phe Gly Gln Leu
370 375 380

His Pro Arg Ser Gln Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser
385 390 395 400

Ser Leu Phe Pro Asn Arg Ala Pro Ala Gly Arg Val Leu Leu Leu Asn
405 410 415

Tyr Ile Gly Gly Ser Thr Asn Thr Gly Ile Val Ser Lys Thr Glu Ser
420 425 430

Asp Leu Val Gly Ala Val Asp Arg Asp Leu Arg Lys Met Leu Ile Asn
435 440 445

Pro Arg Ala Ala Asp Pro Leu Ala Leu Gly Val Arg Val Trp Pro Gln
450 455 460

Ala Ile Pro Gln Phe Leu Ile Gly His Leu Asp Arg Leu Ala Ala Ala
465 470 475 480

Lys Ser Ala Leu Gly Gln Gly Gly Tyr Asp Gly Leu Phe Leu Gly Gly
485 490 495

Asn Tyr Val Ala Gly Val Ala Leu Gly Arg Cys Ile Glu Gly Ala Tyr
500 505 510

Glu Ser Ala Ser Gln Val Ser Asp Phe Leu Thr Lys Tyr Ala Tyr Lys

515 520 525

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1647 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 55..1683
(D) OTHER INFORMATION: /product= "soybean protox-1 cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

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CTTTAGCACA GTGTTGAAGA TAACGAACGA ATAGTGCCAT TACTGTAACC AACC ATG        57
                                                          Met
                                                          355

GTT TCC GTC TTC AAC GAG ATC CTA TTC CCG CCG AAC CAA ACC CTT CTT       105
Val Ser Val Phe Asn Glu Ile Leu Phe Pro Pro Asn Gln Thr Leu Leu
            360                 365                 370

CGC CCC TCC CTC CAT TCC CCA ACC TCT TTC TTC ACC TCT CCC ACT CCA       153
Arg Pro Ser Leu His Ser Pro Thr Ser Phe Phe Thr Ser Pro Thr Arg
        375                 380                 385

AAA TTC CCT CGC TCT CCC CCT AAC CCT ATT CTA CGC TGC TCC ATT GCG       201
Lys Phe Pro Arg Ser Arg Pro Asn Pro Ile Leu Arg Cys Ser Ile Ala
    390                 395                 400

GAG GAA TCC ACC GCG TCT CCG CCC AAA ACC AGA GAC TCC GCC CCC GTG       249
Glu Glu Ser Thr Ala Ser Pro Pro Lys Thr Arg Asp Ser Ala Pro Val
405                 410                 415

GAC TGC GTC GTC GTC GGC GGA GGC GTC AGC GGC CTC TGC ATC GCC CAG       297
Asp Cys Val Val Val Gly Gly Gly Val Ser Gly Leu Cys Ile Ala Gln
420                 425                 430                 435

GCC CTC GCC ACC AAA CAC GCC AAT GCC AAC GTC GTC GTC ACG GAG GCC       345
Ala Leu Ala Thr Lys His Ala Asn Ala Asn Val Val Val Thr Glu Ala
            440                 445                 450

CGA GAC CGC GTC GGC GGC AAC ATC ACC ACG ATG GAG ACG GAC GGA TAC       393
Arg Asp Arg Val Gly Gly Asn Ile Thr Thr Met Glu Arg Asp Gly Tyr
        455                 460                 465

CTC TGG GAA GAA GGC CCC AAC AGC TTC CAG CCT TCT GAT CCA ATG GTC       441
Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu
    470                 475                 480

ACC ATC GTG GTC GAC AGT GCT TTA AAG GAT GAG CTT GTT TTG GGG GAT       489
Thr Met Val Val Asp Ser Gly Leu Lys Asp Glu Leu Val Leu Gly Asp
485                 490                 495
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     GAT GCA CCT CGG TTT GTG TTG TGG AAC AGC AAG TTG AGG CCG GTG        537
Pro Asp Al  Pro Arg Phe Val Leu Trp Asn Arg Lys Leu Arg Pro Val
500                 505                 510                 515

CCC GGG AAG CTG ACT GAT TTG CCT TTC TTT GAC TTG ATG AGC ATT GGT        585
Pro Gly Lys Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile Gly
                520                 525                 530

GGC AAA ATC AGG GCT GGC TTT GGT GCG CTT GGA ATT CCG CCT CCT CCT        633
Gly Lys Ile Arg Ala Gly Phe Gly Ala Leu Gly Ile Arg Pro Pro Pro
            535                 540                 545

CCA GGT CAT GAG GAA TCG GTT GAA GAG TTT GTT CGT CGG AAC CTT GGT        681
Pro Gly His Glu Glu Ser Val Glu Glu Phe Val Arg Arg Asn Leu Gly
        550                 555                 560

GAT GAG GTT TTT GAA CGG TTG ATA GAG CCT TTT TGT TCA GGG GTC TAT        729
Asp Glu Val Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr
    565                 570                 575

GCA GGC GAT CCT TCA AAA TTA AGT ATG AAA GCA GCA TTC GGG AAA GTT        777
Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly Lys Val
580                 585                 590                 595

TGG AAG CTG GAA AAA AAT GGT GGT AGC ATT ATT GGT GGA ACT TTC AAA        825
Trp Lys Leu Glu Lys Asn Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys
                600                 605                 610

GCA ATA CAA GAG AGA AAT GGA GCT TCA AAA CCA CCT CGA GAT CCG CCT        873
Ala Ile Gln Glu Arg Asn Gly Ala Ser Lys Pro Pro Arg Asp Pro Arg
            615                 620                 625

CTG CCA AAA CCA AAA GGT CAG ACT GTT GGA TCT TTC CGG AAG GGA CTT        921
Leu Pro Lys Pro Lys Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu
        630                 635                 640

ACC ATG TTG CCT GAT GCA ATT TCT GCC AGA CTA GGC AAC AAA GTA AAG        969
Thr Met Leu Pro Asp Ala Ile Ser Ala Arg Leu Gly Asn Lys Val Lys
    645                 650                 655

TTA TCT TGG AAG CTT TCA AGT ATT AGT AAA CTG GAT AGT GGA GAG TAC       1017
Leu Ser Trp Lys Leu Ser Ser Ile Ser Lys Leu Asp Ser Gly Glu Tyr
660                 665                 670                 675

AGT TTG ACA TAT GAA ACA CCA GAA GGA GTG CTT TCT TTG CAG TGC AAA       1065
Ser Leu Thr Tyr Glu Thr Pro Glu Gly Val Val Ser Leu Gln Cys Lys
                680                 685                 690

ACT GTT GTC CTG ACC ATT CCT TCC TAT GTT GCT AGT ACA TTG CTG CGT       1113
Thr Val Val Leu Thr Ile Pro Ser Tyr Val Ala Ser Thr Leu Leu Arg
            695                 700                 705

CCT CTG TCT GCT GCT GCT GCA GAT GCA CTT TCA AAG TTT TAT TAC CCT       1161
Pro Leu Ser Ala Ala Ala Ala Asp Ala Leu Ser Lys Phe Tyr Tyr Pro
        710                 715                 720

CCA GTT GCT GCA GTT TCC ATA TCC TAT CCA AAA GAA GCT ATT AGA TCA       1209
Pro Val Ala Ala Val Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg Ser
    725                 730                 735

GAA TGC TTG ATA GAT GGT GAG TTG AAG GGG TTC GGT CAA TTG CAT CCA       1257
Glu Cys Leu Ile Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro
                                46
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     7                   745                 750                 755

     CGT AGC CAA GGA GTG GAA ACA TTA GGA ACT ATA TAC AGC TCA TCA CTA      1305
     Arg Ser Gln Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu
                     760                 765                 770

     TTC CCC AAC CGA GCA CCA CCT GGA AGG GTT CTA CTC TTG AAT TAC ATT      1353
     Phe Pro Asn Arg Ala Pro Pro Gly Arg Val Leu Leu Leu Asn Tyr Ile
                 775                 780                 785

     GGA GCA GCA ACT AAT ACT GGA ATT TTA TCG AAG ACG GAC AGT GAA CTT      1401
     Gly Gly Ala Thr Asn Thr Gly Ile Leu Ser Lys Thr Asp Ser Glu Leu
             790                 795                 800

     GTG GAA ACA GTT GAT CGA GAT TTC AGG AAA ATC CTT ATA AAC CCA AAT      1449
     Val Glu Thr Val Asp Arg Asp Leu Arg Lys Ile Leu Ile Asn Pro Asn
         805                 810                 815

     GCC CAG GAT CCA TTT GTA GTG GGG GTG AGA CTG TGG CCT CAA GCT ATT      1497
     Ala Gln Asp Pro Phe Val Val Gly Val Arg Leu Trp Pro Gln Ala Ile
     820                 825                 830                 835

     CCA CAG TTC TTA GTT GGC CAT CTT GAT CTT CTA GAT GTT GCT AAA GCT      1545
     Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu Asp Val Ala Lys Ala
                 840                 845                 850

     TCT ATC AGA AAT ACT GGG TTT GAA GGG CTC TTC CTT GGG GGT AAT TAT      1593
     Ser Ile Arg Asn Thr Gly Phe Glu Gly Leu Phe Leu Gly Gly Asn Tyr
             855                 860                 865

     GTG TCT GGT GTT GCC TTG GCA CGA TGC GTT GAG GGA GCC TAT GAG CTA      1641
     Val Ser Gly Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Val
         870                 875                 880

     GCA GCT GAA GTA AAC GAT TTT CTC ACA AAT AGA GTG TAC AAA              1683
     Ala Ala Glu Val Asn Asp Phe Leu Thr Asn Arg Val Tyr Lys
     885                 890                 895

     TAGTAGCAGT TTTTCTTTTT GTGGTGGAAT GGGTGATGGG ACTCTCGTGT TCCATTGAAT    1743

     TATAATAATG TGAAAGTTTC TCAAATTCGT TCGATAGGTT TTTGCCGGCT TCTATTGCTC    1803

     ATAATGTAAA ATCCTCTTTA AGTTTGAAAA AAAAAAAAA AAAA                      1847

(2) INFORMATION FOR SEQ ID NO:12:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 543 amino acids
              (B) TYPE: amino acid
              (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein

        (xi) SEQUENCE DESCRIPTION: SEQ ID 12:

     Met Val Ser Val Phe Asn Glu Ile Leu Phe Pro Pro Asn Gln Thr Leu
       1               5                  10                  15

     Leu Arg Pro Ser Leu His Ser Pro Thr Ser Phe Phe Thr Ser Pro Thr
                  20                  25                  30

     Arg Lys Phe Pro Arg Ser Arg Pro Asn Pro Ile Leu Arg Cys Ser Ile
                                     47
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                35                  40                  45
Ala Glu Glu Ser Thr Ala Ser Pro Pro Lys Thr Arg Asp Ser Ala Pro
     50                  55                  60
Val Asp Cys Val Val Val Gly Gly Gly Val Ser Gly Leu Cys Ile Ala
 65                  70                  75                  80
Gln Ala Leu Ala Thr Lys His Ala Asn Ala Asn Val Val Val Thr Glu
                 85                  90                  95
Ala Arg Asp Arg Val Gly Gly Asn Ile Thr Thr Met Glu Arg Asp Gly
            100                 105                 110
Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met
        115                 120                 125
Leu Thr Met Val Val Asp Ser Gly Leu Lys Asp Glu Leu Val Leu Gly
    130                 135                 140
Asp Pro Asp Ala Pro Arg Phe Val Leu Trp Asn Arg Lys Leu Arg Pro
145                 150                 155                 160
Val Pro Gly Lys Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile
                165                 170                 175
Gly Gly Lys Ile Arg Ala Gly Phe Gly Ala Leu Gly Ile Arg Pro Pro
            180                 185                 190
Pro Pro Gly His Glu Glu Ser Val Glu Glu Phe Val Arg Arg Asn Leu
        195                 200                 205
Gly Asp Glu Val Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly Val
    210                 215                 220
Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly Lys
225                 230                 235                 240
Val Trp Lys Leu Glu Lys Asn Gly Gly Ser Ile Ile Gly Gly Thr Phe
                245                 250                 255
Lys Ala Ile Gln Glu Arg Asn Gly Ala Ser Lys Pro Pro Arg Asp Pro
            260                 265                 270
Arg Leu Pro Lys Pro Lys Gly Gln Thr Val Gly Ser Phe Arg Lys Gly
        275                 280                 285
Leu Thr Met Leu Pro Asp Ala Ile Ser Ala Arg Leu Gly Asn Lys Val
    290                 295                 300
Lys Leu Ser Trp Lys Leu Ser Ser Ile Ser Lys Leu Asp Ser Gly Glu
305                 310                 315                 320
Tyr Ser Leu Thr Tyr Glu Thr Pro Glu Gly Val Val Ser Leu Gln Cys
                325                 330                 335
Lys Thr Val Val Leu Thr Ile Pro Ser Tyr Val Ala Ser Thr Leu Leu
            340                 345                 350
Arg Pro Leu Ser Ala Ala Ala Ala Asp Ala Leu Ser Lys Phe Tyr Tyr
        355                 360                 365
Pro Pro Val Ala Ala Val Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg
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370 375 380

Ser Glu Cys Leu Ile Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His
385 390 395 400

Pro Arg Ser Gln Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser
405 410 415

Leu Phe Pro Asn Arg Ala Pro Pro Gly Arg Val Leu Leu Leu Asn Tyr
420 425 430

Ile Gly Gly Ala Thr Asn Thr Gly Ile Leu Ser Lys Thr Asp Ser Glu
435 440 445

Leu Val Glu Thr Val Asp Arg Asp Leu Arg Lys Ile Leu Ile Asn Pro
450 455 460

Asn Ala Gln Asp Pro Phe Val Val Gly Val Arg Leu Trp Pro Gln Ala
465 470 475 480

Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu Asp Val Ala Lys
485 490 495

Ala Ser Ile Arg Asn Thr Gly Phe Glu Gly Leu Phe Leu Gly Gly Asn
500 505 510

Tyr Val Ser Gly Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu
515 520 525

Val Ala Ala Glu Val Asn Asp Phe Leu Thr Asn Arg Val Tyr Lys
530 535 540

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 583 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:
(A) NAME/KEY: promoter
(B) LOCATION: 1..583
(D) OTHER INFORMATION: /function= "arabidopsis protox-1 promoter"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAATTCCGAT CGAATTATAT AATTATCATA AATTTGAATA AGCATGTTCC CTTTTATTAA 60

AGAGTTTTAA TAAAGTTTGC TAATAATGCA CTTTCACTTC AAACTCGATT CTCATGTAAT 120

TAATTAATAT TTACATCAAA ATTTGGTCAC TAATATTACC AAATTAATAT ACTAAAATGT 180

TAATTCGCAA ATAAAACACT AATTCCAAAT AAAGGTCAT TATGATAAAC ACGTATTGAA 240

CTTGATAAAG CAAAGCAAAA ATAATGGGTT TCAAGGTTTG GGTTATATAT GACAAAAAAA 300

AAAAAGTTT TGGTTATATA TCTATTGGGC CTATAACCAT GTTATACAAA TTTGGGCCTA 360

ACTAAAATAA TAAAATAAAC GTAATGGTCC TTTTTATATT TGGGTCAAAC CCAACTCTAA 420

ACCCAAACCA AAGAAAAAGT ATACGGTACG GTACACAGAC TTATGGTGTG TGTGATTGCA 480

GGTGAATATT TCTCGTCGTC TTCTCCTTTC TTCTGAAGAA GATTACCCAA TCTGAAAAAA 540

ACCAAGAAGC TGACAAAATT CCGAATTCTC TGCGATTTCC ATG 583

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1048 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCGATCTTTC TAGGCTGATC CCCAAATCTT CCTCGGAAGC CCCTGGCGCC TCTGCCCCTT 60

GGAGCTGGTG GCCTGAAAGA GCTTTGCTGT TGCCCCGAAG ATTGTGAGGT ATATTGTGAC 120

CTCTGAGACT GACTTCCTTT GTCGTCACTT TGAGTGGAGT TATGGATTGA CCTGACGTGC 180

CTCAGATGGA TTCTTCCTCC GAAGCCCCTG GTCATTTCGG AGAATCTGTA ATCTTATTCC 240

CTTCTTTGGC GAAAATCTGT CAGCTTGGAT GTACTCATCC ATCTTCTGAA GCAGCTTCTC 300

CAGAGTTTGT GGAGGCTTCC TGGCGAAATA TTGGGCTGTA GGTCCTGGAC GAAGACCCTT 360

GATCATGGCC TCAATGAGAA TCTCATTGGG CACCGTAGGC GCTTGTGCCC TCAATCGCAA 420

GAACCTTCGT ACATATGCCT GAAGGTATTC TTCGTGATCT TGTGTGCATT GGAACAGAGC 480

CTGAGCTGTG ACCGACTTCG TTTGAAAGCC TTGGAAGCTA GTAACCAACA TGTGCTTAAG 540

CTTCTGCCAC GACGTGATAG TCCCTGGCCG AAGAGAAGAA TACCATGTTT GGGCTACATT 600

CCGGACTGCC ATGACGAAGG ACTTCGCCAT GACTACAGTG TTGACCCCAT ACGAAGATAT 660

ACTTGCTTCG TAGCTCATCA GAAACTGCTT TGGATCTGAG TGCCCATCAT ACATGGGGAG 720

CTGAGGTGGC TTGTATGATC GGAACCATGG GGTAGCCTGC AGTTCTGCTG CCAAGGAGA 780

AGCATCATCA AAAGTAAAGG CATCATGATT AAAATCATCA TACCATCCAT CCTCGTTGAA 840

TAAGCCTTCT TGACGAAGCT CCCTGTGTTG GGGCCTTCGA TCTTGTTCAT CTTGAACAAG 900

ATGACGCACT TCTTCAGTGG CTTCGTCGAT CTTTCTTTGG AGATCAGCCA GTCGCACCAT 960

CTTCTCGTTC TTTCTTTGTA CTTGTTTATG GATGATCTCC ATGTCCCTAA TCTCTTGGTC 1020

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CAACTCCTCC TCTTGGAGTG TCAGACTGGT GGCTTTCCTC TTCTGGCTTC GAGCCTCTCG 1080
GAGAAAGA GTTTCTTGAT TTGGGTCCAG CGGCTGCAGT GCAGTGGTCC CTGGTGCTGA 1140
AGCTTTCTTC GGTGGCATGA CAAAGGTCAG TGCTTGCCGA AGGTGGTCGA AAAGGGTTCA 1200
CTAGAGGTGG GAGCCAATGT TGGGGACTTC TCAAGTGCTA TGAGTTAAGA ACAAGGCAAC 1260
ACAAAATGTT AAATATTAAT AGCTTTCATC TTTCGAAGCA TTATTTCCCT TTGGGTATAA 1320
TGATCTTCAG ACGAAAGAGT CCTTCATCAT TGCGATATAT GTTAATAGAA GGAGGAGCAT 1380
ATGAAATGTA AGAGACAACA TGAACAATCG TGTAGCATTG TTAATTCATC ATCATTTTAT 1440
TATTATGGAA AAATAGAAAC AATATTGAAT TACAAATGTA CCTTTGGCTT GACAGAAGAT 1500
AAAAGTACAA GCTTGACGCA CGAGCAAGTA CAAGTCAGTG TGAACAGTAC GGGGTACTG 1560
TTCATCTATT TATAGGCACA GGACACAGCC TGTGAGAAAT TACAGTCATG CCCTTTACAT 1620
TTACTATTGA CTTATAGAAA AATCTATCAG GACTGGATAG CCTTTTCCCC TTTAAGTCGG 1680
TGCCTTTTTC CGCGATTAAG CCGAATCTCC CTTGCGCATA GCTTCGGAGC ATCGGCAACC 1740
TTCGTCACGA TCATGCCCTT CTCATTGTGT ATGCTTTTAA TCCTGAATTC GAAGGTACCT 1800
GTCCATAAAC CATACTTGGA AGACATTGTT AAATTATGTT TTTGAGGACC TTCGGAGGAC 1860
GAAGGCCCCC AACAGTCGTG TTTTTGAGGA CCTTCGGAAG ATGAAGGCCC CCAACAAGAC 1920
CTATCCATAA AACCAACCTA TCCACAAAAC CGACCCCATT CACCCTTCAT TTGCCTCACC 1980
AACAACCCTA ATTAGGTTGT TGGTTTAAAT TTTTTAGGGT CAATTTGGTC ATCACCATCC 2040
ACTGTCACTC CACAAACTCA AATCAATAA ACAGACTCAA TCACCCAAAC TGACCATACC 2100
CATAAAACCG CCCCACCCTT CTAGCGCCTC GCCAGAAACC AGAAACCCTG ATTCAGAGTT 2160
CAAACTTAAA ACGACCATAA CTTTCACCTT GGAACTCGAA TCAGGTCCAT TTTTTTCCAA 2220
ATCACACAAA ATTAAATTTC GCATCCGATA ATCAAGCCAT CTCTTCACTA TGGTTTTAAG 2280
TGTTGCTCAC ACTAGTGTAT TTATGGACTA ATCACCTGTG TATCTCATAC AATAACATAT 2340
CAGTACATCT AAGTTGTTAC TCAATTACCA AAACCGAATT ATAGCCTTCG AAAAAGGTTA 2400
TCGACTAGTC ACTCAATTAC CAAAACTAAA CTTTAGACTT TCATGTATGA CATCCAACAT 2460
GACACTGTAC TGGACTAAAC CACCTTTCAA GCTACACAAG GAGCAAAAAT AACTAAT.TT 2520
CGTAGTTGTA GGAGCTAAAG TATATGTCCA CAACAATAGT TAAGGGAAGC CCCCAAGGAC 2580
TTAAAACTCC TTTTACCTCT TGAAACTTTT GTCGTGGTCT ACTTTTTCAC TTTAAACTTC 2640
AAAATTTGAC ATTTTATCAC CCCTTAACTC TTAAAACCAT TTAAATTACA TTCTTACTAG 2700
ATTATAGATG ATTTTGTTGT GAAAAGTTTT TAAGACATGT TTACACATTG ATTAAAATCA 2760
TTTGTTCAAT TTCCTAGAGT TAAATCTAAT CTTATTAAAA CTATTAGAGA TACTTTCACG 2820
AGCTCTAAAT ATTTTTATTT TTTCATTATG GAATTTTGTT AGAATTCTTA TAGACCTTTT 2880
TTTGTGGTTT AAAAGCCTTG CCATGTTTTT AACAAGTTTT TTTTCTATTT TTTGAAATTT 2940

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      TTGGAAAC CACTTCTAAC GCGGTAGAAG ATTTATTTTG CTACACTTAT ATCTACAACA   3000
      AAATCAACTT ATGAAATTGT CTTGGAAACT ACCTCTAACC CGGTAGAATG AATTTGAATG   3060
      AAAATTAAAC CAACTTACGG AATCGCCCAA CATATGTCGA TTAAAGTGGA TATGGATACA   3120
      TATGAAGAAG CCCTAGAGAT AATCTAAATG GTTTCAGAAT TGAGGGTTAT TTTTTGAAGT   3180
      TTGATGGGAA GATAAGACCA TAACGGTAGT TCACAGAGAT AAAAGGGTTA TTTTTTTCAG   3240
      AAATATTTGT GCTGCAATTG ATCCTGTGCC TCAAATTCAG CCTGCAACCA AGGCCAGTTT   3300
      CTAGAGCGAA CAAGCCCAC GTCACCCGTG GCCCGTCAGG CGAAGCAGCT CTTGTGCAGA   3360
      CTTTGAGAGG GATTGGATAT CAACGGAACC AATCACGCAC GGCAATGCGA TTCCCAGCCC   3420
      ACCTGTAACG TTCGAGTGGG CCATCCTTAA CTCCAAGCCC AACGGCCCTA CCCCATCTCG   3480
      TCGTGTCATC CACTCCGCCG CACAGGCGCT CAGCTCCGCA ACGCCGCCGG AAATGGTCGC   3540
      CGCCACAGCC ACCGCCATGG CCACCGCTGC ATCGCCGCTA CTCAACGGGA CCCGAATACC   3600
      TCCGCCCCTC CGCCATCGAG GACTCAGCGT GCGCTGCGCT GCTGTGGCGG GCGGCGCGGC   3660
      CGAGGCACCG GCATCCACCG GCGCGCGGCT GTCCGCGGAC TGCGTTGTGG TGGGCGGAGG   3720
      CATCAGTGGC CTCTGCACCG CGCAGGCGCT GGCCACGCGG CACGGCGTCG GGGAGGTGCT   3780
      TGTCACGGAG GCCCGCGCCC GCCCCGGCGG CAACATTACC ACCGTCGAGC GCCCCGAGCA   3840
      AGGGTACC                                                           3848
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The invention as described herein is contemplated to include the following enumerated embodiments:

1. A recombinant DNA molecule comprising a plant protoporphyrinogen oxidase (protox) promoter or a functionally equivalent derivative thereof.

2. A chimeric gene comprising a plant protox promoter operably linked to a heterologous DNA coding sequence.

3. The chimeric gene of claim 2 wherein said plant protox promoter is from a protox-1 gene.

4. The chimeric gene of claim 2 wherein said plant protox promoter is from a protox-2 gene.

5. The chimeric gene of claim 2 wherein said protox promoter is from a plant selected from the group consisting of *Arabidopsis*, soybean, cotton, tobacco, sugar beet, oilseed rape, maize, wheat, sorghum, rye, oats, turf grass and rice.

6. The chimeric gene of claim 5 wherein said promoter is from a plant selected from the group consisting of *Arabidopsis* and maize.

7. The chimeric gene of claim 6 wherein said promoter is at least 300 nucleotides in length.

8. The chimeric gene of claim 7 wherein said promoter is at least 500 nucleotides in length.

9. The chimeric gene of claim 8 wherein said promoter is from *Arabidopsis* and has the sequence set forth in SEQ ID No. 13.

10. The chimeric gene of claim 8 wherein said promoter is from maize and has the sequence set forth in SEQ ID No. 14.

11. The chimeric gene of claim 2 wherein said heterologous coding sequence encodes a modified, herbicide-resistant form of a plant enzyme.

12. The chimeric gene of claim 11 wherein said plant enzyme is selected from the group consisting of imidazoleglycerol phosphate dehyratase (IGPD), EPSP synthase, glutamine synthetase (GS), acetyl coenzyme A carboxylase, acetolactate synthase, and protoporphyrinogen oxidase (protox).

13. The chimeric gene of claim 12 wherein said plant enzyme is protox.

14. A recombinant DNA vector comprising the recombinant DNA molecule of claim 1.

15. Plant tissue comprising the chimeric gene of claim 2.

16. A plant comprising the chimeric gene of claim 2.

17. The plant of claim 16 wherein said plant is selected from the group consisting of *Arabidopsis*, soybean, cotton, tobacco, sugar beet, oilseed rape, maize, wheat, sorghum, rye, oats, turf grass and rice.

ABSTRACT OF DISCLOSURE

Promoters naturally associated with plant protoporphyrinogen oxidase (protox) coding sequences, and derivatives thereof, are provided. These promoters can be used to control the expression of an operably linked heterologous coding sequence in a plant cell. . These promoters are particularly useful for expressing modified forms of herbicide target enzymes, particularly modified forms of protox, to achieve tolerance to herbicides which inhibit the corresponding unmodified enzymes. Recombinant DNA molecules and chimeric genes comprising these promoters are provided, as well as plant tissue and plants containing such chimeric genes.